

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 21:20:54 ; Search time 1915.63 Seconds
(without alignments)
229.406 Million cell updates/sec

Title: US-10-037-990A-3
Perfect score: 21
Sequence: 1 gtcgtgcagcctccagagacc 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 21

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database :

- 1: gb_da:*
- 2: gb_htg:*
- 3: gb_in:*
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- 13: gb_un:*
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- 27: em_sts:*
- 28: em_un:*
- 29: em_vl:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query No. Score Match Length DB ID Description

1	21	100.0	21	6	AX147016	Sequence
2	21	100.0	27	6	BD000273	Sequence
3	21	100.0	48	6	AX003946	Sequence
4	21	100.0	48	6	AX003947	Sequence
5	21	100.0	48	6	AX021565	Sequence
6	21	100.0	48	6	AX021566	Sequence
7	21	100.0	48	6	AX021575	Sequence
8	21	100.0	48	6	AX021576	Sequence
9	21	100.0	48	6	AX021631	Sequence
10	21	100.0	48	6	AX021632	Sequence

ALIGNMENTS

RESULT	1	AX147016	21 bp	DNA	linear	PAT 08-JUN-2001
LOCUS	AX147016	Sequence	10	from Patent	WO0137291.	
DEFINITION	AX147016	Sequence	10	from Patent	WO0137291.	
ACCESSION	AX147016	Sequence	10	from Patent	WO0137291.	
VERSION	AX147016.1	GI:14346287				
KEYWORDS		synthetic construct.				
SOURCE		synthetic construct				
ORGANISM		artificial sequence.				
REFERENCE	1	(bases 1 to 21)				
AUTHORS	Weindel,K., Riedling,M. and Geiger,A.					
TITLE	Magnetic glass particles, method for their preparation and uses thereof					
JOURNAL	Patent: WO 0137291-A 10 25-MAY-2001;					
FEATURES	Roche Diagnostics GmbH (DE)					
source	Location/Qualifiers					
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	/db_xref="taxon:32630"					
	/note="Synthetic oligonucleotide probe (HCV)"					
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	/note="Ruthenium+-(tris-bipyridyl)-derivatisation"					
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ORIGIN						

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QY 1 gtcgtgcagcctccagagacc 21
DB 1 gtcgtgcagcctccagagacc 21

RESULT 2
BD000273/c 27 bp DNA linear PAT 31-JAN-2002
LOCUS BD000273
DEFINITION Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof.
ACCESSION BD000273
VERSION BD000273.1 GI:18623352
KEYWORDS JP 2000279200-A/11.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 27)
AUTHORS Lyden,J.M. and Gorman,K.M.
TITLE Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof
JOURNAL Patent: JP 2000279200-A 11 10-OCT-2000;
ORIGIN ORTHO CLINICAL DIAGNOSTICS INC
COMMENT OS Artificial Sequence
PN JP 2000279200-A/11
PD 10-OCT-2000
PF 03-FEB-2000 JP 2000032656

Re: 101037990

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtcgtcagcctccagagacc 21
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DB 10 GTCGTGACGCTCCAGAGACC 30

RESULT 7
AX021575 48 bp DNA linear PAT 07-SEP-2000
LOCUS AX021575
DEFINITION Sequence 13 from Patent WO9924606.
ACCESSION AX021575
VERSION AX021575.1 GI:10044859
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.

REFERENCE
AUTHORS Kessler,C., Bartl,K., Habermussen,G. and Orum,H.
TITLE Specific and sensitive nucleic acid detection method
PATENT: WO 9924606-A 13 20-MAY-1999;
JOURNAL KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);
ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)

FEATURES
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Location/Qualifiers
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/db_xref="taxon:32630"
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BASE COUNT 9 a 18 c 14 g 7 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtcgtcagcctccagagacc 21
|||||
DB 10 GTCGTGACGCTCCAGAGACC 30

RESULT 8
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LOCUS AX021576
DEFINITION Sequence 14 from Patent WO9924606.
ACCESSION AX021576
VERSION AX021576.1 GI:10044860
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.

REFERENCE
AUTHORS Kessler,C., Bartl,K., Habermussen,G. and Orum,H.
TITLE Specific and sensitive nucleic acid detection method
PATENT: WO 9924606-A 14 20-MAY-1999;
JOURNAL KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);
ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)

FEATURES
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Location/Qualifiers
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BASE COUNT 9 a 17 c 14 g 8 t
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Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtcgtcagcctccagagacc 21
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DB 10 GTCGTGACGCTCCAGAGACC 30

RESULT 9
AX021631 48 bp DNA linear PAT 07-SEP-2000
LOCUS AX021631
DEFINITION Sequence 10 from Patent WO9923250.
ACCESSION AX021631
VERSION AX021631.1 GI:10044914
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.

REFERENCE
AUTHORS Kessler,C., Bartl,K., Habermussen,G. and Orum,H.
TITLE Specific and sensitive method for detecting nucleic acids
PATENT: WO 9923250-A 10 14-MAY-1999;
JOURNAL KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);
ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)

FEATURES
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Location/Qualifiers
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/db_xref="taxon:32630"
/note="HCV_2B"

BASE COUNT 9 a 18 c 14 g 7 t
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Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtcgtcagcctccagagacc 21
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DB 10 GTCGTGACGCTCCAGAGACC 30

RESULT 10
AX021632 48 bp DNA linear PAT 07-SEP-2000
LOCUS AX021632
DEFINITION Sequence 11 from Patent WO9923250.
ACCESSION AX021632
VERSION AX021632.1 GI:10044915
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.

REFERENCE
AUTHORS Kessler,C., Bartl,K., Habermussen,G. and Orum,H.
TITLE Specific and sensitive method for detecting nucleic acids
PATENT: WO 9923250-A 11 14-MAY-1999;
JOURNAL KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);
ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)

FEATURES
SOURCE
1. 48
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="HCV_MCR"

BASE COUNT 9 a 17 c 14 g 8 t
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Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtcgtcagcctccagagacc 21
|||||

Tue Aug 27 15:49:52 2002

us-10-037-990a-3.oli.rge

Page 4

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Search completed: August 26, 2002, 21:20:54
Job time: 7708 sec

Result No.	Query Match	Length	DB	ID	Description
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2	21	100.0	27	6	BD000273	Oligonuc
3	21	100.0	48	6	AX003846	Sequence
4	21	100.0	48	6	AX003947	Sequence
5	21	100.0	48	6	AX021565	Sequence
6	21	100.0	48	6	AX021566	Sequence
7	21	100.0	48	6	AX021575	Sequence
8	21	100.0	48	6	AX021576	Sequence
9	21	100.0	48	6	AX021631	Sequence
10	21	100.0	48	6	AX021632	Sequence

ALIGNMENTS

RESULT	1			
LOCUS	AX147016	21 bp	DNA	linear
DEFINITION	Sequence...10. from Patent WO0137291.			
ACCESSION	AX147016			
VERSION	AX147016.1	GI:14346287		
PAT	08-JUN-2001			

REFERENCE 1 (bases 1 to 21)

AUTHORS	TITLE
Weinidel, K., Riedling, M. and Geiger, A.	Magnetic glass particles, method for their preparation and uses thereof

JOURNAL Patent: WO 0137291-A 10 25-MAY-2001
Roche Diagnostics GmbH (DE)
FEATURES Location/Qualifiers

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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide probe (HCV)"
modified_base
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BASE COUNT	3 a	9 c	6 g	3 o
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Query Match	100.0%	Score 21:	DB 6:	Length 21:
Best Local Similarity	100.0%	Pred. No.	0.042:	
Matches 21:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:

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QY 1 gtcgtgcagcctcaggacc 21
    |||
Db 1 gtcgtgcagcctcaggacc 21
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RESULT 2	14-00000
BD000273/C	DATE 31-JAN-2002
*****	PAGE 01

LOCUS	2 / bp	DNA	linear	PAI 31-2-2000
BD000273				
DEFINITION	Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof.			

ACCESSION	BD000273
VERSION	BD000273.1 GI:18623352
KEYWORDS	JP 2000279200-A/11.

SOURCE ORGANISM	
synthetic construct	
synthetic construct	
artificial sequence	

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 1 to 27)	Lyneen, J.M. and Gorman, K.M.	Oligonucleotide primers for efficient virus (HCV) and methods of use thereof	Patent: JP 2000279200-A 11 10-OCT-2000

COMMENT	OS	Artificial Sequence
	PN	JP 2000279200-A/11
	PD	10-OCT-2000
	PF	03-FEB-2000 JP 2000032656

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```
RESULT 2
AAH25408
ID AAH25408 standard; DNA: 21 BP.
XX
AC AAH25408;
XX
DT 22-AUG-2001 (first entry)
XX
DE Detection probe for a HCV DNA fragment.
XX
KM Magnetic glass particle; nucleic acid purification; probe; ss.
XX
OS Hepatitis C virus.
XX
FH Key 1 Location/Qualifiers
FT modified_base 1
FT /tag= "a
FT /note= "ruthenium3+-(tris-bipyridyl)-derivatisation"
PN W0200137291-A1.
XX
PD 25-MAY-2001.
XX
PE 17-NOV-2000; 2000MO-EP11459.
XX
PR 17-NOV-1999; 99EP-0122853.
PR 12-MAY-2000; 2000EP-0110165.
XX
PA (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI Weindel K, Riedling M, Geiger A;
XX
DR WPI; 2001-381247/40.
XX
PT Novel composition of magnetic glass particles for purification of DNA
PT or RNA in automated processes
XX
PS Example 7; Page 96; 105pp; English.
XX
CC The specification describes a composition of magnetic glass particles,
CC which contain at least one magnetic object with a mean diameter between
CC 5-500 nm. The composition is useful for the purification of nucleic
CC acids. The composition can be used to process large quantities of
CC nucleic acid samples, because it does not involve the particles being
CC centrifuged or the fluids being drawn through glass fiber filters.
CC The present sequence represents a probe for a HCV DNA fragment. The
CC DNA fragment can be purified using the method of the invention.
XX
SO Sequence 21 BP; 3 A; 9 C; 6 G; 3 T; 0 other:

Query Match 100.0%; Score 21; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtcgtcagccctccagacc 21
DB 1 gtcgtcagccctccagacc 21

RESULT 3
AA064928/C
ID AA064928 standard; DNA: 22 BP.
XX
AC AA064928;
XX
DT 19-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense.
XX
```

```
KW therapy; inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PE 23-AUG-1993; 93CA-2104649.
XX
PR 25-AUG-1992; 92JP-0248796.
PR 03-MAR-1993; 93JP-0042736.
XX
PA (SEKI/) SEKI M.
XX
PI Honda Y, Seki M, Yamada E;
XX
DR WPI; 1994-151836/19.
XX
PT Antl:sense oligo:nucleotide(s) complementary to the hepatitis C
PT virus genome - are useful as antiviral agents
XX
PS Claim 5; Page 70; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound
CC i.e. it has a base sequence of 16-24 bases which is included
CC within the 24 bases from G at position 127 to C at position 150 of
CC AA064913 and which contains at least 16 bases from C at position 131
CC to A at position 146. The antisense oligonucleotide is useful for
CC inhibiting translation of HCV genes.
XX
SO Sequence 22 BP; 3 A; 6 C; 10 G; 3 T; 0 other:

Query Match 100.0%; Score 21; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtcgtcagccctccagacc 21
DB 22 gtcgtcagccctccagacc 2

RESULT 4
AA064932/C
ID AA064932 standard; DNA: 22 BP.
XX
AC AA064932;
XX
DT 19-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KM therapy; inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PE 23-AUG-1993; 93CA-2104649.
XX
PR 25-AUG-1992; 92JP-0248796.
PR 03-MAR-1993; 93JP-0042736.
XX
PA (SEKI/) SEKI M.
XX
PI Honda Y, Seki M, Yamada E;
XX
DR WPI; 1994-151836/19.
XX
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PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
virus genome - are useful as antiviral agents
XX
XX
PS Claim 5; Page 72; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound
CC 1.e. it has a base sequence of 16-24 bases which is included
CC within the 24 bases from G at position 127 to C at position 150 of
CC AA064933 and which contains at least 16 bases from C at position 131
CC to A at position 146. The antisense oligonucleotide is useful for
CC inhibiting translation of HCV genes.
XX
SQ Sequence 22 BP; 4 A; 6 C; 9 G; 3 T; 0 other;

Query Match 100.0%; Score 21; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.076; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtcgtcagcctccagacc 21
|||||
DB 21 GTCGTGACGCTCCAGACC 1

RESULT 5
AA064933/C
ID AA064933 standard; DNA; 23 BP.
XX
XX AA064933;
AC
DT 19-DEC-1994 (first entry)
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
DE
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW therapy; inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX CA2104649-A.
PN
XX 26-FEB-1994.
PD
XX 23-AUG-1993; 93CA-2104649.
PF
XX 25-AUG-1992; 92JP-0248796.
PR 03-MAR-1993; 93JP-0042736.
XX
XX (SEKI/) SEKI M.
PA
XX
XX Honda Y, Seki M, Yamada E;
PI
XX WPI: 1994-151836/19.
DR
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
virus genome - are useful as antiviral agents
PT
XX
XX Claim 5; Page 72; 262pp; English.
PS
XX This oligonucleotide is an example of a preferred antisense compound
CC 1.e. it has a base sequence of 16-24 bases which is included
CC within the 24 bases from G at position 127 to C at position 150 of
CC AA064933 and which contains at least 16 bases from C at position 131
CC to A at position 146. The antisense oligonucleotide is useful for
CC inhibiting translation of HCV genes.
XX
SQ Sequence 23 BP; 4 A; 6 C; 10 G; 3 T; 0 other;

Query Match 100.0%; Score 21; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.076; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtcgtcagcctccagacc 21
|||||
DB 22 GTCGTGACGCTCCAGACC 2

RESULT 6
AA064937/C
ID AA064937 standard; DNA; 23 BP.
XX
XX AA064937;
AC
XX
XX 19-DEC-1994 (first entry)
DT
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
DE
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW therapy; inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX CA2104649-A.
PN
XX 26-FEB-1994.
PD
XX 23-AUG-1993; 93CA-2104649.
PF
XX 25-AUG-1992; 92JP-0248796.
PR 03-MAR-1993; 93JP-0042736.
XX
XX (SEKI/) SEKI M.
PA
XX
XX Honda Y, Seki M, Yamada E;
PI
XX WPI: 1994-151836/19.
DR
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
virus genome - are useful as antiviral agents
PT
XX
XX Claim 5; Page 74; 262pp; English.
PS
XX This oligonucleotide is an example of a preferred antisense compound
CC 1.e. it has a base sequence of 16-24 bases which is included
CC within the 24 bases from G at position 127 to C at position 150 of
CC AA064933 and which contains at least 16 bases from C at position 131
CC to A at position 146. The antisense oligonucleotide is useful for
CC inhibiting translation of HCV genes.
XX
SQ Sequence 23 BP; 4 A; 7 C; 9 G; 3 T; 0 other;

Query Match 100.0%; Score 21; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.076; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtcgtcagcctccagacc 21
|||||
DB 21 GTCGTGACGCTCCAGACC 1

RESULT 7
AA064938/C
ID AA064938 standard; DNA; 24 BP.
XX
XX AA064938;
AC
XX
XX 19-DEC-1994 (first entry)
DT
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
DE
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW therapy; inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS

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XX CA2104649-A.
XX
XX 26-FEB-1994.
XX
XX 23-AUG-1993; 93CA-2104649.
XX
XX 25-AUG-1992; 93JP-0248796.
XX
XX 03-MAR-1993; 93JP-0042736.
XX
XX (SEKI/) SEKI M.
XX
XX Honda Y, Seki M, Yamada E;
XX
XX WPI; 1994-151836/19.
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
XX virus genome - are useful as antiviral agents
XX
XX Claim 5; Page 75; 262pp; English.
XX
XX This oligonucleotide is an example of a preferred antisense compound
XX i.e. it has a base sequence of 16-24 bases which is included
XX within the 24 bases from G at position 127 to C at position 150 of
XX AA04913 and which contains at least 16 bases from C at position 131
XX to A at position 146. The antisense oligonucleotide is useful for
XX inhibiting translation of HCV genes.
XX
XX Sequence 24 BP; 4 A; 7 C; 10 G; 3 T; 0 Other;
XX
OY Query Match 100.0%; Score 21; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY 1 gtcgtcagccttcagacc 21
DB 22 gtcgtcagccttcagacc 2

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PS	Claim 5; Page 117; 262pp; English.
XX	This oligonucleotide is an example of a preferred antisense compound
CC	i.e. it has a base sequence of 15-30 bases which is included
CC	within the 49 bases from G at position 127 to C at position 175 of
CC	AA064913 and which contains at least 7 bases from C at position 147
CC	to C at position 153. The antisense oligonucleotide is useful for
CC	inhibiting translation of HCV genes.
XX	
SO	Sequence 25 BP; 3 A; 6 C; 13 G; 3 T; 0 other;
Query Match	100.0%; Score 21; DB 15; Length 25;
Best Local Similarity	100.0%; Pred. No. 0.076;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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DB	25 gtccgacgacctccaggacc 5
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ID	AA065030/c
XX	AA065030 standard; DNA: 26 BP.
AC	
XX	AA065030;
DT	20-DEC-1994 (first entry)
XX	
DE	Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX	
RW	Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW	therapy; inhibition; viral protein precursor; ss.
XX	
OS	Synthetic.
XX	
PN	CA2104649-A.
PD	26-FEB-1994.
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PF	23-AUG-1993; 93CA-2104649.
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PR	25-AUG-1992; 92JP-0248796.
PR	03-MAR-1993; 93JP-0042736.
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PA	(SEKI/) SEKI M.
PI	
DR	Honda Y, Seki M, Yamada E;
WP	1994-151836/19.
XX	
PT	Anti-sense oligo:nucleotide(s) complementary to the hepatitis C
XX	virus genome - are useful as antiviral agents
PS	
CS	Claim 5; Page 115; 262pp; English.
XX	
CC	This oligonucleotide is an example of a preferred antisense compound
CC	i.e. it has a base sequence of 15-30 bases which is included
CC	within the 49 bases from G at position 127 to C at position 175 of
CC	AA064913 and which contains at least 7 bases from C at position 147
CC	to C at position 153. The antisense oligonucleotide is useful for
CC	inhibiting translation of HCV genes.
XX	
SO	Sequence 26 BP; 4 A; 6 C; 13 G; 3 T; 0 other;
Query Match	100.0%; Score 21; DB 15; Length 26;
Best Local Similarity	100.0%; Pred. No. 0.076;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 gtcgtgcagctccaggacc 21
DB	25 gtccgacgacctccaggacc 5

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RESULT 10
AA065036/C
ID AA065036 standard: DNA; 26 BP.
XX
XX
AC AA065036;
XX
XX
DT 20-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C virus genome.
XX
KM Hepatitis C virus; Non-A, non-B hepatitis virus; HCV; antisense;
KM therapy; inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PM CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-2104649.
XX
PR 25-AUG-1992; 92JP-0248796.
PR 03-MAR-1993; 93JP-0042736.
XX
PA (SEKI/) SEKI M.
XX
PI Honda Y, Seki M, Yamada E;
XX
DR WPI: 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
XX virus genome - are useful as antiviral agents
XX
PS Claim 5; Page 117; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound
CC 1.e. it has a base sequence of 15-30 bases which is included
CC within the 49 bases from G at position 127 to C at position 175 of
CC AA064913 and which contains at least 7 bases from C at position 147
CC to C at position 153. The antisense oligonucleotide is useful for
CC inhibiting translation of HCV genes.
XX
SQ Sequence 26 BP; 4 A; 6 C; 13 G; 3 T; 0 other;

Query Match 100.0%; Score 21; DB 15; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtcgtgcagcctccagacc 21
DB 26 gtcgtgcagcctccagacc 6

RESULT 11
AA065026/C
ID AA065026 standard: DNA; 27 BP.
XX
XX
AC AA065026;
XX
XX
DT 20-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C virus genome.
XX
KM Hepatitis C virus; Non-A, non-B hepatitis virus; HCV; antisense;
KM therapy; inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PM CA2104649-A.
XX
```

```
PD 26-FEB-1994.
XX
XX
PF 23-AUG-1993; 93CA-2104649.
XX
PR 25-AUG-1992; 92JP-0248796.
PR 03-MAR-1993; 93JP-0042736.
XX
XX
PA (SEKI/) SEKI M.
XX
PI Honda Y, Seki M, Yamada E;
XX
DR WPI: 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
XX virus genome - are useful as antiviral agents
XX
PS Claim 5; Page 113; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound
CC 1.e. it has a base sequence of 15-30 bases which is included
CC within the 49 bases from G at position 127 to C at position 175 of
CC AA064913 and which contains at least 7 bases from C at position 147
CC to C at position 153. The antisense oligonucleotide is useful for
CC inhibiting translation of HCV genes.
XX
SQ Sequence 27 BP; 4 A; 7 C; 13 G; 3 T; 0 other;

Query Match 100.0%; Score 21; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtcgtgcagcctccagacc 21
DB 25 gtcgtgcagcctccagacc 5

RESULT 12
AA065031/C
ID AA065031 standard: DNA; 27 BP.
XX
XX
AC AA065031;
XX
XX
DT 20-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C virus genome.
XX
KM Hepatitis C virus; Non-A, non-B hepatitis virus; HCV; antisense;
KM therapy; inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PM CA2104649-A.
XX
PN 26-FEB-1994.
XX
PD 23-AUG-1993; 93CA-2104649.
XX
PF 25-AUG-1992; 92JP-0248796.
PR 03-MAR-1993; 93JP-0042736.
XX
XX
PA (SEKI/) SEKI M.
XX
PI Honda Y, Seki M, Yamada E;
XX
DR WPI: 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
XX virus genome - are useful as antiviral agents
XX
PS Claim 5; Page 115; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound
```

CC 1.e. It has a base sequence of 15-30 bases which is included
CC within the 49 bases from G at position 127 to C at position 175 of
CC AA064913 and which contains at least 7 bases from C at position 147
CC to C at position 153. The antisense oligonucleotide is useful for
CC inhibiting translation of HCV genes.

XX Sequence 27 BP; 5 A; 6 C; 13 G; 3 T; 0 other;

Query Match 100.0%; Score 21; DB 15; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.075;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtcgtcagcctccagagacc 21

DB 26 gtcgtcagcctccagagacc 6

RESULT 13

AA065037/C

ID AA065037 standard; DNA; 27 BP.

XX AA065037;

XX 20-DEC-1994 (first entry)

XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.

XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;

KW therapy; inhibition; viral protein precursor; ss.

XX Synthetic.

XX CA2104649-A.

XX 26-FEB-1994.

XX 23-AUG-1993; 93CA-2104649.

XX 25-AUG-1992; 92JP-0248796.

PR 03-MAR-1993; 93JP-0042736.

XX (SEKI/) SEKI M.

XX Honda Y, Seki M, Yamada E;

DR WPI; 1994-151836/19.

XX Anti-sense oligo:nucleotide(s) complementary to the hepatitis C

PT virus genome - are useful as antiviral agents

XX Claim 5; Page 118; 262pp; English.

XX This oligonucleotide is an example of a preferred antisense compound

CC 1.e. It has a base sequence of 15-30 bases which is included

CC within the 49 bases from G at position 127 to C at position 175 of

CC AA064913 and which contains at least 7 bases from C at position 147

CC to C at position 153. The antisense oligonucleotide is useful for

CC inhibiting translation of HCV genes.

XX Sequence 27 BP; 4 A; 6 C; 14 G; 3 T; 0 other;

Query Match 100.0%; Score 21; DB 15; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.075;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtcgtcagcctccagagacc 21

DB 27 gtcgtcagcctccagagacc 7

RESULT 14

AAA74629/C

ID AAA74629 standard; DNA; 27 BP.

XX AAA74629;

XX 08-JAN-2001 (first entry)

XX HCV probe C96-22-PRB.

XX Hepatitis C virus; HCV; HCV detection; probe; ss.

XX Hepatitis C virus.

XX Epi026262-A2.

XX 09-AUG-2000.

XX 01-FEB-2000; 2000EP-0300763.

XX 03-FEB-1999; 99US-0118497.

XX (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.

XX Linen JM, Gorman KM;

XX WPI; 2000-507254/46.

XX Detecting hepatitis C virus in biological sample involves amplifying

PT reverse transcribed products of virus RNA using amplification primers

PT whose sequences correspond to 5' or 3' non-coding region of the virus

XX Claim 30; Page 27; 28pp; English.

XX The present sequence is a probe used in a method for detecting hepatitis

CC C virus (HCV) RNA in biological samples. The HCV RNA is reverse

CC transcribed to generate cDNA. This is then amplified with primers

CC corresponding to the 5' or 3' non-coding region of HCV. The product

CC was captured by hybridisation to oligonucleotide probes, including the

CC present sequence, which were covalently attached to latex particles and

CC deposited on the surface of a flow through membrane. The probe/product

CC complex was reacted with streptavidin-horseradish peroxidase conjugate,

CC which catalyses the oxidative conversion of a dye precursor to a blue

CC dye. The method is useful for the diagnosis of HCV infection in

CC patients, in testing the efficacy of anti-HCV therapeutic regimes, and

CC in screening blood for HCV-infected samples. The method provides an

CC improved single-round, reverse transcription/amplification assay which

CC detects low copy levels of HCV RNA. The primers and assay system are

CC designed to allow the co-amplification of multiple regions of the HCV

CC genome, multiple viral species, and an internal positive control (IPC)

CC RNA (or DNA). Simultaneous amplification/detection of multiple regions

CC of the HCV genome increases assay sensitivity and the co-amplification

CC of an IPC decreases the likelihood of false negative results because of

XX PCR inhibition.

XX Sequence 27 BP; 5 A; 8 C; 9 G; 5 T; 0 other;

Query Match 100.0%; Score 21; DB 21; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.075;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtcgtcagcctccagagacc 21

DB 21 gtcgtcagcctccagagacc 1

RESULT 15

AA065038/C

ID AA065038 standard; DNA; 28 BP.

XX AA065038;

DT 20-DEC-1994 (first entry)
 XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
 DE Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
 XX therapy; inhibition; viral protein precursor; ss.
 KM Synthetic.
 XX
 OS CA2104649-A.
 PN
 XX
 XX 26-FEB-1994.
 PD
 XX
 XX 23-AUG-1993; 93CA-2104649.
 PF
 XX 25-AUG-1992; 92JP-0248796.
 PR 03-MAR-1993; 93JP-0042736.
 XX
 XX (SEKI/) SEKI M.
 PA
 XX
 PI Honda Y, Seki M, Yamada E;
 XX WPI: 1994-151836/19.
 DR
 XX
 XX Antisense oligo:nucleotide(s) complementary to the hepatitis C
 PT virus genome - are useful as antiviral agents
 PS Claim 5; Page 118; 262pp; English.
 CC
 XX This oligonucleotide is an example of a preferred antisense compound
 CC 1.e. it has a base sequence of 15-30 bases which is included
 CC within the 49 bases from G at position 127 to C at position 175 of
 CC AA064913 and which contains at least 7 bases from C at position 147
 CC to C at position 153. The antisense oligonucleotide is useful for
 CC inhibiting translation of HCV genes.
 CC
 SQ Sequence 28 BP; 4 A; 6 C; 15 G; 3 T; 0 other;

Query Match 100.0%; Score 21; DB 15; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.075;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtcgtcagcctccagacc 21
 ||||||||||||||||
 DB 28 gtcgtcagcctccagacc 8

RESULT 16
 AA065027/C
 ID AA065027 standard; DNA; 28 BP.
 XX
 AC AA065027;
 XX
 DT 20-DEC-1994 (first entry)
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
 XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
 KM therapy; inhibition; viral protein precursor; ss.
 XX
 OS Synthetic.
 XX
 PN CA2104649-A.
 XX
 XX 26-FEB-1994.
 PD
 XX
 XX 23-AUG-1993; 93CA-2104649.
 PF
 XX 25-AUG-1992; 92JP-0248796.
 PR 03-MAR-1993; 93JP-0042736.
 XX
 XX (SEKI/) SEKI M.
 PA

XX
 PI Honda Y, Seki M, Yamada E;
 XX WPI: 1994-151836/19.
 DR
 XX
 XX Antisense oligo:nucleotide(s) complementary to the hepatitis C
 PT virus genome - are useful as antiviral agents
 PS Claim 5; Page 113; 262pp; English.
 CC
 XX This oligonucleotide is an example of a preferred antisense compound
 CC 1.e. it has a base sequence of 15-30 bases which is included
 CC within the 49 bases from G at position 127 to C at position 175 of
 CC AA064913 and which contains at least 7 bases from C at position 147
 CC to C at position 153. The antisense oligonucleotide is useful for
 CC inhibiting translation of HCV genes.
 CC
 SQ Sequence 28 BP; 5 A; 7 C; 13 G; 3 T; 0 other;

Query Match 100.0%; Score 21; DB 15; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.075;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtcgtcagcctccagacc 21
 ||||||||||||||||
 DB 26 gtcgtcagcctccagacc 6

RESULT 17
 AA065032/C
 ID AA065032 standard; DNA; 28 BP.
 XX
 AC AA065032;
 XX
 DT 20-DEC-1994 (first entry)
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
 XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
 KM therapy; inhibition; viral protein precursor; ss.
 XX
 OS Synthetic.
 XX
 PN CA2104649-A.
 PD
 XX
 XX 26-FEB-1994.
 PF
 XX 23-AUG-1993; 93CA-2104649.
 PR 25-AUG-1992; 92JP-0248796.
 PR 03-MAR-1993; 93JP-0042736.
 XX
 XX (SEKI/) SEKI M.
 PA
 XX
 PI Honda Y, Seki M, Yamada E;
 XX WPI: 1994-151836/19.
 DR
 XX
 XX Antisense oligo:nucleotide(s) complementary to the hepatitis C
 PT virus genome - are useful as antiviral agents
 PS Claim 5; Page 116; 262pp; English.
 CC
 XX This oligonucleotide is an example of a preferred antisense compound
 CC 1.e. it has a base sequence of 15-30 bases which is included
 CC within the 49 bases from G at position 127 to C at position 175 of
 CC AA064913 and which contains at least 7 bases from C at position 147
 CC to C at position 153. The antisense oligonucleotide is useful for
 CC inhibiting translation of HCV genes.
 CC
 SQ Sequence 28 BP; 5 A; 6 C; 14 G; 3 T; 0 other;

Query Match 100.0%; Score 21; DB 15; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.075;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtctgagcctccagacc 21
 |||||
 DB 27 GTCGTGACCTCCAGACCC 7

RESULT 18

AA065039/C
 ID AA065039 standard; DNA: 29 BP.

AC AA065039;

DT 20-DEC-1994 (first entry)

DE Antisense oligonucleotide complementary to Hepatitis C virus genome.

KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
 KM therapy: inhibition; viral protein precursor; ss.

XX Synthetic.

PN CA2104649-A.

PD 26-FEB-1994.

PF 23-AUG-1993; 93CA-2104649.

PR 25-AUG-1992; 92JP-0248796.

PR 03-MAR-1993; 93JP-0042736.

XX (SEKI/) SEKI M.

PI Honda Y, Seki M, Yamada E;

DR WPI; 1994-151836/19.

PT Antisense oligo:nucleotide(s) complementary to the hepatitis C

PS Claim 5; Page 119; 262pp; English.

CC This oligonucleotide is an example of a preferred antisense compound

CC i.e. it has a base sequence of 15-30 bases which is included

CC within the 49 bases from G at position 127 to C at position 175 of

CC AA064913 and which contains at least 7 bases from C at position 147

CC to C at position 153. The antisense oligonucleotide is useful for

CC inhibiting translation of HCV genes.

SO Sequence 29 BP; 4 A; 6 C; 16 G; 3 T; 0 other;

OY 1 gtctgagcctccagacc 21
 |||||

DB 29 GTCGTGACCTCCAGACCC 9

RESULT 19

AA065028/C
 ID AA065028 standard; DNA: 29 BP.

AC AA065028;

DT 20-DEC-1994 (first entry)

DE Antisense oligonucleotide complementary to Hepatitis C virus genome.

XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
 KM therapy: inhibition; viral protein precursor; ss.

XX Synthetic.

PN CA2104649-A.

PD 26-FEB-1994.

PF 23-AUG-1993; 93CA-2104649.

PR 25-AUG-1992; 92JP-0248796.

PR 03-MAR-1993; 93JP-0042736.

XX (SEKI/) SEKI M.

PI Honda Y, Seki M, Yamada E;

DR WPI; 1994-151836/19.

PT Antisense oligo:nucleotide(s) complementary to the hepatitis C

PS Claim 5; Page 114; 262pp; English.

CC This oligonucleotide is an example of a preferred antisense compound

CC i.e. it has a base sequence of 15-30 bases which is included

CC within the 49 bases from G at position 127 to C at position 175 of

CC AA064913 and which contains at least 7 bases from C at position 147

CC to C at position 153. The antisense oligonucleotide is useful for

CC inhibiting translation of HCV genes.

SO Sequence 29 BP; 5 A; 7 C; 14 G; 3 T; 0 other;

OY 1 gtctgagcctccagacc 21
 |||||

DB 27 GTCGTGACCTCCAGACCC 7

RESULT 20

AA065033/C
 ID AA065033 standard; DNA: 29 BP.

AC AA065033;

DT 20-DEC-1994 (first entry)

DE Antisense oligonucleotide complementary to Hepatitis C virus genome.

KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
 KM therapy: inhibition; viral protein precursor; ss.

XX Synthetic.

PN CA2104649-A.

PD 26-FEB-1994.

PF 23-AUG-1993; 93CA-2104649.

PR 25-AUG-1992; 92JP-0248796.

PR 03-MAR-1993; 93JP-0042736.

XX (SEKI/) SEKI M.

PI Honda Y, Seki M, Yamada E;

DR WPI: 1994-151836/19.
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT virus genome - are useful as antiviral agents
XX
XX
PS Claim 5; Page 116; 262pp; English.
XX
XX This oligonucleotide is an example of a preferred antisense compound
CC 1.e. it has a base sequence of 15-30 bases which is included
CC within the 49 bases from G at position 127 to C at position 175 of
CC AA064913 and which contains at least 7 bases from C at position 147
CC to C at position 153. The antisense oligonucleotide is useful for
CC inhibiting translation of HCV genes.
XX
SQ Sequence 29 BP; 5 A; 6 C; 15 G; 3 T; 0 other;

Query Match 100.0%; Score 21; DB 15; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 gtcgtcagcctccaggacc 21
DB 28 gtcgtcagcctccaggacc 8

RESULT 21
AA065040/C
ID AA065040 standard; DNA; 30 BP.
XX
XX AA065040;
XX
XX 20-DEC-1994 (first entry)
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
DE
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW therapy; inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX CA2104649-A.
XX
XX 26-FEB-1994.
XX
XX 23-AUG-1993; 93CA-2104649.
XX
XX 25-AUG-1992; 92JP-0248796.
XX
XX 03-MAR-1993; 93JP-0042736.
XX
XX (SEKI/) SEKI M.
XX
XX Honda Y, Seki M, Yamada E;
XX
XX WPI: 1994-151836/19.
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT virus genome - are useful as antiviral agents
XX
XX
PS Claim 5; Page 119; 262pp; English.
XX
XX This oligonucleotide is an example of a preferred antisense compound
CC 1.e. it has a base sequence of 15-30 bases which is included
CC within the 49 bases from G at position 127 to C at position 175 of
CC AA064913 and which contains at least 7 bases from C at position 147
CC to C at position 153. The antisense oligonucleotide is useful for
CC inhibiting translation of HCV genes.
XX
SQ Sequence 30 BP; 4 A; 7 C; 16 G; 3 T; 0 other;

Query Match 100.0%; Score 21; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 gtcgtcagcctccaggacc 21
DB 28 gtcgtcagcctccaggacc 8

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 gtcgtcagcctccaggacc 21
DB 30 gtcgtcagcctccaggacc 10

RESULT 22
AA065029/C
ID AA065029 standard; DNA; 30 BP.
XX
XX AA065029;
XX
XX 20-DEC-1994 (first entry)
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
DE
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW therapy; inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX CA2104649-A.
XX
XX 26-FEB-1994.
XX
XX 23-AUG-1993; 93CA-2104649.
XX
XX 25-AUG-1992; 92JP-0248796.
XX
XX 03-MAR-1993; 93JP-0042736.
XX
XX (SEKI/) SEKI M.
XX
XX Honda Y, Seki M, Yamada E;
XX
XX WPI: 1994-151836/19.
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT virus genome - are useful as antiviral agents
XX
XX
PS Claim 5; Page 114; 262pp; English.
XX
XX This oligonucleotide is an example of a preferred antisense compound
CC 1.e. it has a base sequence of 15-30 bases which is included
CC within the 49 bases from G at position 127 to C at position 175 of
CC AA064913 and which contains at least 7 bases from C at position 147
CC to C at position 153. The antisense oligonucleotide is useful for
CC inhibiting translation of HCV genes.
XX
SQ Sequence 30 BP; 5 A; 7 C; 15 G; 3 T; 0 other;

Query Match 100.0%; Score 21; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 gtcgtcagcctccaggacc 21
DB 28 gtcgtcagcctccaggacc 8

RESULT 23
AA065034/C
ID AA065034 standard; DNA; 30 BP.
XX
XX AA065034;
XX
XX 20-DEC-1994 (first entry)
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
DE
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW therapy; inhibition; viral protein precursor; ss.

XX OS Synthetic.
XX PN CA2104649-A.
XX PD 26-FEB-1994.
XX PF 23-AUG-1993; 93CA-2104649.
XX PR 25-AUG-1992; 92JP-0248796.
XX PR 03-MAR-1993; 93JP-0042736.
XX PA (SEKI/) SEKI M.
XX PI Honda Y, Seki M, Yamada E;
XX DR WPI: 1994-151836/19.
XX PT Anti-sense oligo:nucleotide(s) complementary to the hepatitis C
XX PT virus genome - are useful as antiviral agents
XX PS Claim 5; Page 116; 262pp; English.
XX CC This oligonucleotide is an example of a preferred antisense compound
XX CC 1.e. it has a base sequence of 15-30 bases which is included
XX CC within the 49 bases from G at position 127 to C at position 175 of
XX CC AA064913 and which contains at least 7 bases from C at position 147
XX CC to C at position 153. The antisense oligonucleotide is useful for
XX CC inhibiting translation of HCV genes.
XX SQ Sequence 30 BP; 5 A; 6 C; 16 G; 3 T; 0 other;

Query Match 100.0%; Score 21; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtcgtcagcctccagacc 21
|||||
DB 29 gtcgtcagcctccagacc 9

RESULT 24
AA23541
ID AA23541 standard; DNA; 48 BP.
XX AC AA23541;
XX DT 21-DEC-1999 (first entry)
XX DE HCV DNA fragment 1.
XX KW Assay; amplification; hybridisation; probe; detection; viral; bacterial;
XX KW cellular; yeast; fungal; primer; ss.
XX OS Hepatitis C virus.
XX PN DE19814828-A1.
XX PD 07-OCT-1999.
XX PF 02-APR-1998; 98DE-1014828.
XX PR 02-APR-1998; 98DE-1014828.
XX PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX PI Kessler C, Habershausen G, Batz H, Oerum H;
XX DR WPI: 1999-552286/47.
XX PT Nucleic acid amplification assay for detecting viral, bacterial,
XX PT cellular, yeast or fungal nucleic acids

XX PS Disclosure; Fig 4; 28pp; German.
XX CC This invention describes a novel assay for a nucleic acid comprises:
XX CC (a) generating amplification products from a fragment of the nucleic
XX CC acid, (b) contacting the amplification products with a probe; and
XX CC (c) detecting hybridization between the amplification product and the
XX CC probe. The assay is useful for detection of viral, bacterial, cellular,
XX CC yeast or fungal nucleic acids in human, animal, bacterial, plant, yeast
XX CC or fungal samples, e.g. feces, smears, cell suspensions, cultures or
XX CC tissue, cell or liquid biopsy samples. This sequence represents a
XX CC fragment of the HCV genome used in the method of the invention.
XX SQ Sequence 48 BP; 9 A; 18 C; 14 G; 7 T; 0 other;

Query Match 100.0%; Score 21; DB 20; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtcgtcagcctccagacc 21
|||||
DB 10 gtcgtcagcctccagacc 30

RESULT 25
AA23542
ID AA23542 standard; DNA; 48 BP.
XX AC AA23542;
XX DT 21-DEC-1999 (first entry)
XX DE Human DNA fragment 1.
XX KW Assay; amplification; hybridisation; probe; detection; viral; bacterial;
XX KW cellular; yeast; fungal; primer; ss.
XX OS Homo sapiens.
XX PN DE19814828-A1.
XX PD 07-OCT-1999.
XX PF 02-APR-1998; 98DE-1014828.
XX PR 02-APR-1998; 98DE-1014828.
XX PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX PI Kessler C, Habershausen G, Batz H, Oerum H;
XX DR WPI: 1999-552286/47.
XX PT Nucleic acid amplification assay for detecting viral, bacterial,
XX PT cellular, yeast or fungal nucleic acids
XX PS Disclosure; Fig 4; 28pp; German.
XX CC This invention describes a novel assay for a nucleic acid comprises:
XX CC (a) generating amplification products from a fragment of the nucleic
XX CC acid, (b) contacting the amplification products with a probe; and
XX CC (c) detecting hybridization between the amplification product and the
XX CC probe. The assay is useful for detection of viral, bacterial, cellular,
XX CC yeast or fungal nucleic acids in human, animal, bacterial, plant, yeast
XX CC or fungal samples, e.g. feces, smears, cell suspensions, cultures or
XX CC tissue, cell or liquid biopsy samples. This sequence represents a
XX CC fragment of the human genome which is used in the method of the
XX CC invention.
XX SQ Sequence 48 BP; 9 A; 17 C; 14 G; 8 T; 0 other;

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OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 20:38:47 ; Search time 119.4 Seconds
(without alignments)
49.374 Million cell updates/sec

Title: US-10-037-990A-1

Perfect score: 24
Sequence: 1 gcagaaagcgtctagccatgagcgt 24

Scoring table: OLIGO.NUC
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size: 21

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database:

Issued_Patents_NA: *
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCRM5.COMB.seq: *
6: /cgn2_6/ptodata/2/ina/Backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	1	US-08-240-547-5
2	24	100.0	24	1	US-08-449-050-17
3	24	100.0	24	1	US-08-332-616A-9
4	24	100.0	24	1	US-08-317-220-9
5	24	100.0	24	1	US-08-675-153-7
6	24	100.0	24	2	US-08-738-928-4
7	24	100.0	24	2	US-08-841-252-7
8	24	100.0	24	2	US-08-881-571-7
9	24	100.0	24	4	US-09-282-034-7
10	24	100.0	26	1	US-08-240-547-6
11	24	100.0	26	2	US-08-738-928-1
12	24	100.0	26	3	US-09-039-866-3
13	23	95.8	24	3	US-09-078-290A-9
14	23	95.8	37	5	PCT-US94-05407-14
15	23	95.8	58	5	PCT-US94-05407-12
16	21	87.5	21	4	US-09-034-205-25
17	21	87.5	21	4	US-08-934-097A-25
18	21	87.5	21	4	US-08-851-588-25
19	21	87.5	21	4	US-09-677-218B-25
20	21	87.5	21	4	US-09-677-192-25

ALIGNMENTS

RESULT 1
US-08-240-547-5

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Sequence 5, Application US/08240547
Patent No. 5527669
GENERAL INFORMATION:
APPLICANT: Resnick, Robert M.
APPLICANT: Young, Karen K.Y.
TITLE OF INVENTION: Primers and Probes for Detection of
TITLE OF INVENTION: Hepatitis C and No. 5527669el Variants
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: U.S.A.
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,547
FILING DATE:
CLASSIFICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/918,844
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sias Ph.D., Stacey R.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-240-547-5

Query Match 100.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcagaaagcgtctagccatgagcgt 24
|||||
Db 1 GCAGAAAGCCTAGCCATGAGCCT 24

RESULT 2
US-08-449-050-17
Sequence 17, Application US/08449050
Patent No. 5561058
GENERAL INFORMATION:
APPLICANT: Gelfand, David
APPLICANT: Myers, Thomas
APPLICANT: Sigma, Christopher
TITLE OF INVENTION: Reagents and Methods for Coupled High
TITLE OF INVENTION: Temperature Reverse Transcription and Polymerase Chain
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,050
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-449-050-17

Query Match 100.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcagaaagcgtcagccatgagcgt 24
|||||
DB 1 GCAGAAAGCGCTAGCCATGCGCT 24

RESULT 3
US-08-332-616A-9
Sequence 9, Application US/08332616A
Patent No. 5620852
GENERAL INFORMATION:
APPLICANT: LIN, LILY
APPLICANT: CIMINO, GEORGE
APPLICANT: ZHU, YU SHENG
TITLE OF INVENTION: NUCLEIC ACID PREPARATION METHODS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,616A
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,545
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: HRI-01202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 397-8338
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-332-616A-9

Query Match 100.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcagaaagcgtcagccatgagcgt 24
|||||
DB 1 GCAGAAAGCGCTAGCCATGCGCT 24

RESULT 4
US-08-317-220-9
Sequence 9, Application US/08317220
Patent No. 5654179
GENERAL INFORMATION:
APPLICANT: LIN, LILY
TITLE OF INVENTION: NUCLEIC ACID PREPARATION METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETER G. CARROLL
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,220
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/044,649
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,545
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/614,921
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: HRI-00542
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-317-220-9

Query Match 100.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcagaaagcgtcagccatgagcgt 24
|||||
DB 1 GCAGAAAGCGCTAGCCATGCGCT 24

RESULT 5
US-08-675-153-7
Sequence 7, Application US/08675153
Patent No. 5677124
GENERAL INFORMATION:

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;
; APPLICANT: Dubois, Dwight
; APPLICANT: Winkler, Matthew
; APPLICANT: Pasloske, Brittan L.
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT VIRAL
; TITLE OF INVENTION: RNA STANDARDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,153
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: AMBI:026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-675-153-7
;
Query Match          100.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 gcagaaagcgtctagccatggcgt 24
DB      1 GCAGAAAGCGCTAGCCATGGCGT 24

RESULT      6
US-08-738-928-4
; Sequence 4, Application US/08738928
; Patent No. 5837442
; GENERAL INFORMATION:
; APPLICANT: Tsang, Sue Y.
; TITLE OF INVENTION: Oligonucleotide Primers for Amplifying
; TITLE OF INVENTION: HCV Nucleic Acid
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/738,928
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
```

```

;
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9263
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-738-928-4
;
Query Match          100.0%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 gcagaaagcgtctagccatggcgt 24
DB      1 GCAGAAAGCGCTAGCCATGGCGT 24

RESULT      7
US-08-841-252-7
; Sequence 7, Application US/08841252
; Patent No. 5919625
; GENERAL INFORMATION:
; APPLICANT: DUBOIS, DWIGHT
; APPLICANT: WINKLER, MATTHEW
; APPLICANT: PASLOSKE, BRITTAN L.
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT VIRAL RNA
; TITLE OF INVENTION: STANDARDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD WHITE & DURKEE
; STREET: P. O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,252
; FILING DATE: 29-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 5,677,124
; FILING DATE: 03-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARK B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: AMBI:026--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-841-252-7
;
Query Match          100.0%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcagaaagcgtcagccatgcgt 24
|||||
Db 1 GCAGAAAGCCTCAGCCATGCGCT 24

RESULT 8
US-08-881-571-7
; Sequence 7, Application US/08881571
; Patent No. 5939262
; GENERAL INFORMATION:
; APPLICANT: Pasloske, Brittan L.
; APPLICANT: Dubois, Dwight
; APPLICANT: Brown, David
; APPLICANT: Minkler, Matthew
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
; TITLE OF INVENTION: AND UTILIZATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/881,571
; APPLICATION NUMBER: Concurrently Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/675,153
; FILING DATE: 03-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,145
; FILING DATE: 03-JUL-1996
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ. ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-881-571-7

Query Match 100.0%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcagaaagcgtcagccatgcgt 24
|||||
Db 1 GCAGAAAGCCTCAGCCATGCGCT 24

RESULT 9
US-09-282-054-7
; Sequence 7, Application US/09282054
; Patent No. 6214982
; GENERAL INFORMATION:
; APPLICANT: Pasloske, Brittan L.
; APPLICANT: Dubois, Dwight

APPLICANT: Brown, David
APPLICANT: Minkler, Matthew
TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
TITLE OF INVENTION: AND UTILIZATION
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282,054
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/881,571
FILING DATE:
APPLICATION NUMBER: US 08/675,153
FILING DATE: 03-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/021,145
FILING DATE: 03-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: AMB1:033
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-282-054-7

Query Match 100.0%; Score 24; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcagaaagcgtcagccatgcgt 24
|||||
Db 1 GCAGAAAGCCTCAGCCATGCGCT 24

RESULT 10
US-08-240-547-6
; Sequence 6, Application US/08240547
; Patent No. 5527669
; GENERAL INFORMATION:
; APPLICANT: Resnick, Robert M.
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Primers and Probes for Detection of
; TITLE OF INVENTION: Hepatitis C and No. 5527669e1 Variants
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,547
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/918,844
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sias Ph.D., Stacey R.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-240-547-6

Query Match 100.0%; Score 24; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcagaaagcgtctagccatgcgt 24
|||||
DB 3 GCAGAAAGCGCTAGCCATGGCGT 26

RESULT 11
US-08-738-928-1
Sequence 1, Application US/08738928
Patent No. 5837442
GENERAL INFORMATION:
APPLICANT: Tsang, Sue Y.
TITLE OF INVENTION: Oligonucleotide Primers for Amplifying
TITLE OF INVENTION: HCV Nucleic Acid
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,928
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 9263
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-738-928-1

Query Match 100.0%; Score 24; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcagaaagcgtctagccatgcgt 24
|||||
DB 1 GCAGAAAGCGCTAGCCATGGCGT 24

RESULT 12
US-09-039-866-3
Sequence 3, Application US/09039866
Patent No. 6001611
GENERAL INFORMATION:
APPLICANT: Wall, Stephen G.
TITLE OF INVENTION: MODIFIED NUCLEIC ACID AMPLIFICATION
TITLE OF INVENTION: PRIMERS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Roche Molecular Systems
STREET: 1080 U.S. Highway 202
CITY: Branchburg
STATE: New Jersey
COUNTRY: United States
ZIP: 08876
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,866
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 1023P
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-039-866-3

Query Match 100.0%; Score 24; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcagaaagcgtctagccatgcgt 24
|||||
DB 1 GCAGAAAGCGCTAGCCATGGCGT 24

RESULT 13
US-09-078-290A-9
Sequence 9, Application US/09078290A
Patent No. 6048696
GENERAL INFORMATION:
APPLICANT: Hoffman, Leslie M.
APPLICANT: Hawkins, Gregory A.
TITLE OF INVENTION: METHOD FOR IDENTIFYING NUCLEIC ACID MOLECULES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady

```

; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/078,290A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 310307,90100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5709
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
; US-09-078-290A-9

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Query Match 95.8%; Score 23; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 cagaagcgctagccatgcgct 24
Db 1 CAGAAAGCGCTAGCCATGCGCT 23

RESULT 14
PCT-US94-05407-14
; Sequence 14, Application PC/TUS9405407
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: "NUCLEIC ACID TAGGED IMMUNOASSAY"
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05407
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/061,694
; FILING DATE: 13-MAY-1993
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
PCT-US94-05407-14

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; Query Match 95.8%; Score 23; DB 5; Length 37;
; Best Local Similarity 100.0%; Pred. No. 6.7e-05;
; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2 cagaagcgctagccatgcgct 24
Db 14 CAGAAAGCGCTAGCCATGCGCT 36

RESULT 15
PCT-US94-05407-12
; Sequence 12, Application PC/TUS9405407
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: "NUCLEIC ACID TAGGED IMMUNOASSAY"
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05407
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/061,694
; FILING DATE: 13-MAY-1993
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
PCT-US94-05407-12

Query Match 95.8%; Score 23; DB 5; Length 58;
Best Local Similarity 100.0%; Pred. No. 6.6e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 cagaagcgctagccatgcgct 24
Db 11 CAGAAAGCGCTAGCCATGCGCT 33

RESULT 16
US-09-034-205-25
; Sequence 25, Application US/09034205
; Patent No. 6194149
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
; TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/034,205
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Macknight, Kamlin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: FORS-03268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-09-034-205-25

Query Match 87.5%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcagaaagcgtctagccatgg 21
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DB 1 GCAGAAAGCGCTAGCCATGG 21

RESULT 17
US-08-934-097A-25
Sequence 25, Application US/08934097A
Patent No. 6210880
GENERAL INFORMATION:
APPLICANT: Lyamichev, Victor I.
APPLICANT: Biow, Mary Ann D.
APPLICANT: Fors, Lance
APPLICANT: Neiri, Bruce P.
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
TITLE OF INVENTION: Structure Probing With Structure-Bridging
TITLE OF INVENTION: Oligonucleotides.
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,097A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Macknight, Kamlin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: FORS-02980
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-08-934-097A-25

Query Match 87.5%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GCAGAAAGCGCTAGCCATGG 21

RESULT 18
US-08-851-588-25
Sequence 25, Application US/08851588
Patent No. 6214545
GENERAL INFORMATION:
APPLICANT: Dong, Fang
APPLICANT: Lyamichev, Victor I.
APPLICANT: Prudent, James R.
APPLICANT: Dahlberg, James E.
APPLICANT: Fors, Lance
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
TITLE OF INVENTION: Structure Probing
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,588
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02777
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-08-851-588-25

Query Match 87.5%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcagaaagcgtctagccatgg 21
|||||
DB 1 GCAGAAAGCGCTAGCCATGG 21

RESULT 19
US-09-677-218B-25
; Sequence 25, Application US/09677218B
; Patent No. 6355437
; GENERAL INFORMATION:
; APPLICANT: Lyamlichev, Victor I.
; ; Brow, Mary Ann D.
; ; Fors, Lance
; ; Neil, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
; ; STRUCTURE-BRIDGING OLIGONUCLEOTIDES
; ;
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/677,218B
; FILING DATE: 02-Oct-2000
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/034,205
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnighl, Karin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-03268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 21 base pairs
; ; TYPE: nucleic acid
; ; STRANDEDNESS: single
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: other nucleic acid
; ; DESCRIPTION: /desc = "DNA"
; ; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-677-218B-25

Query Match 87.5%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcagaaagcgtctagccatg 21
| | | | | | | | | | | | | | | | | | | | |
Db 1 GCAGAAAGCGTCTAGCCATG 21

RESULT 20
US-09-677-192-25
; Sequence 25, Application US/09677192
; Patent No. 6358691
; GENERAL INFORMATION:
; APPLICANT: Lyamlichev, Victor I.
; ; Brow, Mary Ann D.
; ; Fors, Lance
; ; Neil, Bruce P.
; APPLICANT: Neil, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING;
; ; FILE REFERENCE: FORS-04708
; ; CURRENT APPLICATION NUMBER: US/09/677,192

; CURRENT FILING DATE: 2000-10-02
; ; PRIOR APPLICATION NUMBER: 09/034,205
; ; PRIOR FILING DATE: 1998-03-03
; ; NUMBER OF SEQ ID NOS: 68
; ; SOFTWARE: PatentIn Ver. 2.0
; ; SEQ ID NO 25
; ; LENGTH: 21
; ; TYPE: DNA
; ; ORGANISM: Artificial Sequence
; ; FEATURE:
; ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-677-192-25

Qy 1 gcagaaagcgtctagccatg 21
| | | | | | | | | | | | | | | | | | | | |
Db 1 GCAGAAAGCGTCTAGCCATG 21

Search completed: August 26, 2002, 22:17:11
Job time: 5904 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 22:17:11 ; Search time 119.4 Seconds
(without alignments)
49.374 Million cell updates/sec

Title: US-10-037-990A-2

Perfect score: 24
Sequence: 1 ctgcgaagcaccctatcagcagcagt 24

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 38353 seqs, 122816752 residues

Word size : 21

Total number of hits satisfying chosen parameters: 41

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database :

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2: /cgn2_6/ptodata/2/ina/5B.COMB.seq: *
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4: /cgn2_6/ptodata/2/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	1 US-08-240-547-18	Sequence 18, Appl
2	24	100.0	24	1 US-08-449-050-16	Sequence 16, Appl
3	24	100.0	24	1 US-08-332-616A-8	Sequence 8, Appl
4	24	100.0	24	1 US-08-317-220-8	Sequence 8, Appl
5	24	100.0	24	1 US-08-675-153-8	Sequence 8, Appl
6	24	100.0	24	1 US-08-244-116B-51	Sequence 51, Appl
7	24	100.0	24	2 US-08-738-928-5	Sequence 5, Appl
8	24	100.0	24	2 US-08-841-252-8	Sequence 8, Appl
9	24	100.0	24	2 US-08-881-571-8	Sequence 8, Appl
10	24	100.0	24	4 US-09-282-054-8	Sequence 8, Appl
11	24	100.0	26	1 US-08-240-547-19	Sequence 19, Appl
12	24	100.0	26	1 US-08-256-568B-4	Sequence 4, Appl
13	24	100.0	26	4 US-09-038-369B-8	Sequence 4, Appl
14	24	100.0	27	5 PCT-US93-00928-1	Sequence 1, Appl
15	24	100.0	28	3 US-08-474-700B-12	Sequence 12, Appl
16	24	100.0	28	5 PCT-US95-05812-12	Sequence 12, Appl
17	24	100.0	33	1 US-08-438-639-51	Sequence 51, Appl
18	24	100.0	33	2 US-07-813-338A-51	Sequence 51, Appl
19	24	100.0	33	2 US-08-470-124-61	Sequence 61, Appl
20	24	100.0	33	3 US-08-441-971-127	Sequence 127, Appl
21	24	100.0	33	4 US-08-221-653-127	Sequence 127, Appl
22	24	100.0	33	4 US-08-442-144A-127	Sequence 127, Appl
23	24	100.0	33	4 US-08-441-970-127	Sequence 127, Appl
24	24	100.0	53	4 US-08-429-181-16	Sequence 16, Appl
25	24	100.0	53	1 US-08-429-181-49	Sequence 49, Appl
26	24	100.0	53	1 US-08-164-388-16	Sequence 16, Appl
27	24	100.0	53	1 US-08-164-388-49	Sequence 49, Appl

C 28	24	100.0	57	1 US-08-356-287-36	Sequence 36, Appl
C 29	24	100.0	57	5 PCT-US93-04863-36	Sequence 36, Appl
C 30	24	100.0	64	1 US-08-429-181-31	Sequence 31, Appl
C 31	24	100.0	64	1 US-08-164-388-31	Sequence 31, Appl
C 32	23	95.8	23	1 US-08-356-287-25	Sequence 25, Appl
C 33	23	95.8	23	5 PCT-US93-04863-25	Sequence 25, Appl
C 34	23	95.8	29	1 US-08-240-547-20	Sequence 20, Appl
C 35	22	91.7	22	1 US-08-356-287-27	Sequence 27, Appl
C 36	22	91.7	22	5 PCT-US93-04863-27	Sequence 27, Appl
C 37	21	87.5	27	2 US-08-738-928-3	Sequence 3, Appl
C 38	21	87.5	28	2 US-08-738-928-2	Sequence 2, Appl
C 39	21	87.5	28	3 US-09-039-866-4	Sequence 4, Appl
C 40	21	87.5	28	3 US-08-474-700B-35	Sequence 35, Appl
C 41	21	87.5	28	5 PCT-US95-05812-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-08-240-547-18
Sequence 18, Application US/08240547
Patent No. 5527669
GENERAL INFORMATION:
APPLICANT: Resnick, Robert M.
TITLE OF INVENTION: Young, Karen K.Y.
TITLE OF INVENTION: Primers and Probes for Detection of
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: U.S.A.
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,547
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/918,844
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sias Ph.D., Stacey R.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-240-547-18

Query Match 100.0% Score 24; DB 1; Length 24;
Best Local Similarity 100.0% Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctgcgaagcaccctatcagcagcagt 24
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Db 1 ctgcgaagcaccctatcagcagcagt 24

RESULT 2
US-08-449-050-16
Sequence 16, Application US/08449050
Patent No. 5561058
GENERAL INFORMATION:
APPLICANT: Gelfand, David
APPLICANT: Myers, Thomas
APPLICANT: Sigua, Christopher
TITLE OF INVENTION: Reagents and Methods for Coupled High
TITLE OF INVENTION: Temperature Reverse Transcription and Polymerase Chain
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,050
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-449-050-16

Query Match 100.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 3,4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctcgaagcaccctatcaggcagt 24
|||||
Db 1 CTCGCAAGCACCCTATCAGGCACT 24

RESULT 3
US-08-332-616A-8
Sequence 8, Application US/08332616A
Patent No. 5620852
GENERAL INFORMATION:
APPLICANT: LIN, LILY
APPLICANT: CIMINO, GEORGE
APPLICANT: ZHU, YU SHENG
TITLE OF INVENTION: NUCLEIC ACID PREPARATION METHODS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,616A
FILING DATE: 31-OCT-1994

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,545
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: HRI-01202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-332-616A-8

Query Match 100.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 3,4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctcgaagcaccctatcaggcagt 24
|||||
Db 1 CTCGCAAGCACCCTATCAGGCACT 24

RESULT 4
US-08-317-220-8
Sequence 8, Application US/08317220
Patent No. 5654179
GENERAL INFORMATION:
APPLICANT: LIN, LILY
TITLE OF INVENTION: NUCLEIC ACID PREPARATION METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETER G. CARROLL
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,220
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/044,649
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,545
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/614,921
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: HRI-00542
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-317-220-8

Query Match
Best Local Similarity 100.0%; Score 24; DB 1; Length 24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagaccctatcaggcagt 24
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Db 1 CTCGCAAGCACCCTATCAGGAGT 24

RESULT 5
US-08-675-153-8
Sequence 8, Application US/08675153
Patent No. 5677124
GENERAL INFORMATION:
APPLICANT: Dubois, Dwight
APPLICANT: Winkler, Matthew
APPLICANT: Pasloske, Brittan L.
TITLE OF INVENTION: RIBONUCLEASE RESISTANT VIRAL
TITLE OF INVENTION: RNA STANDARDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675.153
FILING DATE: Concurrently Herewith
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: AMB1:026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-675-153-8

Query Match
Best Local Similarity 100.0%; Score 24; DB 1; Length 24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagaccctatcaggcagt 24
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Db 1 CTCGCAAGCACCCTATCAGGAGT 24

RESULT 6
US-08-244-116B-51/C
Sequence 51, Application US/08244116B
Patent No. 5763159
GENERAL INFORMATION:

APPLICANT: Simmonds, Peter
APPLICANT: Chan, Shiu-Wan
APPLICANT: Yap, Peng L.
TITLE OF INVENTION: Hepatitis-C Virus Testing
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson, P.A.
STREET: 1211 East Morehead Street
CITY: Charlotte
STATE: No. 5763159th Carolina
COUNTRY: United States
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244.116B
FILING DATE: 15-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02143
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 1749-125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 704-377-1561
TELEFAX: 704-334-2014
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA
DESCRIPTION: oligonucleotide"
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Hepatitis-C virus
US-08-244-116B-51

Query Match
Best Local Similarity 100.0%; Score 24; DB 1; Length 24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagaccctatcaggcagt 24
|||||
Db 24 CTCGCAAGCACCCTATCAGGAGT 1

RESULT 7
US-08-738-928-5
Sequence 5, Application US/08738928
Patent No. 5837442
GENERAL INFORMATION:
APPLICANT: Teang, Sue Y.
TITLE OF INVENTION: Oligonucleotide Primers for Amplifying
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,928
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 9253
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-738-928-5

Query Match 100.0%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctcgcaagcaccctatcaggcagt 24
|||||
DB 1 CTCGCAAGCACCTATCAGGCACT 24

RESULT 8
US-08-841-252-8
Sequence 8, Application US/08841252
Patent No. 5919625
GENERAL INFORMATION:
APPLICANT: DUBOIS, DWIGHT
APPLICANT: WINKLER, MATTHEW
APPLICANT: PASLOSKE, BRITTAN L.
TITLE OF INVENTION: RIBONUCLEASE RESISTANT VIRAL RNA
TITLE OF INVENTION: STANDARDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/841,252
FILING DATE: 29-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 5,677,124
FILING DATE: 03-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: AMBI:026--1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-300
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-841-252-8

Query Match 100.0%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctcgcaagcaccctatcaggcagt 24
|||||
DB 1 CTCGCAAGCACCTATCAGGCACT 24

RESULT 9
US-08-881-571-8
Sequence 8, Application US/08881571
Patent No. 5939262
GENERAL INFORMATION:
APPLICANT: Pasloske, Brittan L.
APPLICANT: Dubois, Dwight
APPLICANT: Brown, David
APPLICANT: Winkler, Matthew
TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
TITLE OF INVENTION: AND UTILIZATION
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,571
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/675,153
FILING DATE: 03-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/021,145
FILING DATE: 03-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: AMBI:033
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-881-571-8

Query Match 100.0%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctcgcaagcaccctatcaggcagt 24
|||||
DB 1 CTCGCAAGCACCTATCAGGCACT 24

RESULT 10
US-09-282-054-8
Sequence 8, Application US/09282054
Patent No. 6214982
GENERAL INFORMATION:
APPLICANT: Pasioloske, Brittan L.
APPLICANT: DUBOIS, Dwight
APPLICANT: Brown, David
APPLICANT: Winkler, Matthew
TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
TITLE OF INVENTION: AND UTILIZATION
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282,054
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/881,571
FILING DATE:
APPLICATION NUMBER: US 08/675,153
FILING DATE: 03-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/021,145
FILING DATE: 03-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: AMB1:033
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-282-054-8

Query Match 100.0%; Score 24; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctgcgaagcaccctatcaggcagt 24
|||||
DB 1 CTCGCAAGCACCCTATCAGGCACT 24

RESULT 11
US-08-240-547-19
Sequence 19, Application US/08240547
Patent No. 3527669
GENERAL INFORMATION:
APPLICANT: Resnick, Robert M.
APPLICANT: Young, Karen K.Y.
TITLE OF INVENTION: Primers and Probes for Detection of
Hepatitis C and No. 5527669e1 Variants
NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: U.S.A.
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,547
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/918,844
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sias Ph.D., Stacey R.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-240-547-19

Query Match 100.0%; Score 24; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctgcgaagcaccctatcaggcagt 24
|||||
DB 3 CTCGCAAGCACCCTATCAGGCACT 26

RESULT 12
US-08-256-568B-4
Sequence 4, Application US/08256568B
Patent No. 5846704
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN.
APPLICANT: ROSSAU, RUDI; VAN HEUVERSUYN, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
TITLE OF INVENTION: ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,568B
FILING DATE: 18-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03325

FILED DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILED DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILED DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: HCV
POSITION IN GENOME: HCV
CHROMOSOME/SEGMENT: HCV
MAP POSITION: Position -29 of 5' end
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..26
OTHER INFORMATION: /standard_name=
US-08-256-569B-4
OTHER INFORMATION: "Universal HCV primer HcPr96"

Query Match 100.0%; Score 24; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ctgcgaagcaccctatcagcagt 24
|||||
Db 3 CTGCAAGCACCTATCAGCAGT 26

RESULT 13
US-09-038-369B-4
Sequence 4, Application US/09038369B
Patent No. 6171784
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT, STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI, VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
TITLE OF INVENTION: ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,369B
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,568

FILED DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILED DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILED DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILED DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: HCV
POSITION IN GENOME: HCV
CHROMOSOME/SEGMENT: HCV
MAP POSITION: Position -29 of 5' end
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..26
OTHER INFORMATION: /standard_name=
US-09-038-369B-4
OTHER INFORMATION: "Universal HCV primer HcPr96"

Query Match 100.0%; Score 24; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ctgcgaagcaccctatcagcagt 24
|||||
Db 3 CTGCAAGCACCTATCAGCAGT 26

RESULT 14
PCT-US93-00928-1
Sequence 1, Application PC/TUS9300928
GENERAL INFORMATION:
APPLICANT: TASSOPOULOS, NIC C.
APPLICANT: HATZAKIS, ANGELOS E.
APPLICANT: KUHN, MARY C.
APPLICANT: TROONEN, HUGO
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS REAGENTS AND ME
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00928
FILED DATE: 19930203
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5132.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-937-9556
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-00928-1

Query Match 100.0%; Score 24; DB 5; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctgcgaagcaccctatcagcagt 24
|||||
Db 3 ctgcgaagcaccctatcagcagt 26

RESULT 15

US-08-474-700B-12
Sequence 12, Application US/08474700B
Patent No. 6001990
GENERAL INFORMATION:
APPLICANT: Wands, Jack
APPLICANT: Wakita, Takeji
APPLICANT: Moradpour, Darius
TITLE OF INVENTION: ANTISENSE INHIBITION OF HEPATITIS C
TITLE OF INVENTION: VIRUS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,700B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,382
FILING DATE: 10 May 1994
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/279001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-474-700B-12

Query Match 100.0%; Score 24; DB 3; Length 28;

Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctgcgaagcaccctatcagcagt 24
|||||
Db 2 ctgcgaagcaccctatcagcagt 25

RESULT 16

PCT-US95-05812-12
Sequence 12, Application PC/TUS9505812
GENERAL INFORMATION:
APPLICANT: Wands, Jack
APPLICANT: Wakita, Takeji
TITLE OF INVENTION: ANTISENSE INHIBITION OF
TITLE OF INVENTION: HEPATITIS C VIRUS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05812
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,382
FILING DATE: 10 May 1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/221001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-05812-12

Query Match 100.0%; Score 24; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctgcgaagcaccctatcagcagt 24
|||||
Db 2 ctgcgaagcaccctatcagcagt 25

RESULT 17

US-08-438-639-51
Sequence 51, Application US/08438639
Patent No. 5712383
GENERAL INFORMATION:
APPLICANT: Sheridan, Patrick
APPLICANT: Chang, Chu-An
APPLICANT: Running, Joyce
APPLICANT: Urdea, Michael S.
TITLE OF INVENTION: PROCESS FOR IMMOBILIZING NUCLEIC ACID
TITLE OF INVENTION: PROBES ON POLYSTYRENE SURFACES

NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION - R440
STREET: P.O. Box 8097
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,639
FILING DATE: 10-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,338
FILING DATE: 23-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Kenneth, M.
REGISTRATION NUMBER: 34,174
REFERENCE/DOCKET NUMBER: 0232.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2719
TELEFAX: (510) 655-3542
TELEX: N/A
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-438-639-51

Query Match 100.0%; Score 24; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcagcgagt 24
|||||
Db 7 CTCGCAAGCACCCTATCAGGCAGT 30

RESULT 18
US-07-813-338A-51
Sequence 51, Application US/07813338A
Patent No. 5747244
GENERAL INFORMATION:
APPLICANT: Sheridan, Patrick
APPLICANT: Chang, Chu-An
APPLICANT: Running, Joyce
APPLICANT: Urdea, Michael S.
TITLE OF INVENTION: PROCESS FOR IMMOBILIZING NUCLEIC ACID
TITLE OF INVENTION: PROBES ON POLYSTYRENE SURFACES
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION - R440
STREET: P.O. Box 8097
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/813,338A
FILING DATE: 23-DEC-1991

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Kenneth, M.
REGISTRATION NUMBER: 34,174
REFERENCE/DOCKET NUMBER: 0232.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2719
TELEFAX: (510) 655-3542
TELEX: N/A
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-813-338A-51

Query Match 100.0%; Score 24; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcagcgagt 24
|||||
Db 7 CTCGCAAGCACCCTATCAGGCAGT 30

RESULT 19
US-08-470-124-61
Sequence 61, Application US/08470124
Patent No. 5849481
GENERAL INFORMATION:
APPLICANT: Urdea, Michael S.
APPLICANT: Horn, Thomas
APPLICANT: Chang, Chu-An
APPLICANT: Warner, Brian
APPLICANT: Fultz, Timothy J.
TITLE OF INVENTION: LARGE COMB-TYPE BRANCHED
TITLE OF INVENTION: POLYNUCLEOTIDES
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 345 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/813,588
FILING DATE: 23 December 1991
ATTORNEY/AGENT INFORMATION:
NAME: Ciotti, Thomas E.
REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 22300-20104.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-470-124-61

Query Match 100.0%; Score 24; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcaggcagt 24
|||||
DB 7 CTCGCAAGCACCCCTATCAGGAGT 30

RESULT 20

US-08-441-971-127
; Sequence 127, Application US/08441971
; Patent No. 6071693

; GENERAL INFORMATION:

; APPLICANT: Tai-An Cha

; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 147

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

; STREET: 600 Atlantic Avenue

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch

; COMPUTER: IBM compatible

; OPERATING SYSTEM: MS-DOS Version 3.3

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/441,971

; FILING DATE: 16-MAY-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/221,653

; FILING DATE:

; APPLICATION NUMBER: US/07/881,528

; FILING DATE:

; APPLICATION NUMBER: 07/697,326

; FILING DATE: 8 May 1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Janiak, Anthony J.

; REGISTRATION NUMBER: 29,809

; REFERENCE/DOCKET NUMBER: C0772/7000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 720-3500

; TELEFAX: (617) 720-2441

; TELEX: EZEKIEL

; INFORMATION FOR SEQ ID NO: 127:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 33 nucleotides

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-08-441-971-127

Query Match 100.0%; Score 24; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcaggcagt 24
|||||
DB 7 CTCGCAAGCACCCCTATCAGGAGT 30

RESULT 21
US-08-221-653-127

; Sequence 127, Application US/08221653
; Patent No. 6190864

; GENERAL INFORMATION:

; APPLICANT: Tai-An Cha

; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 147

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

; STREET: 600 Atlantic Avenue

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch

; COMPUTER: IBM compatible

; OPERATING SYSTEM: MS-DOS Version 3.3

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/221,653

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/881,528

; FILING DATE:

; APPLICATION NUMBER: 07/697,326

; FILING DATE: 8 May 1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Janiak, Anthony J.

; REGISTRATION NUMBER: 29,809

; REFERENCE/DOCKET NUMBER: C0772/7000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 720-3500

; TELEFAX: (617) 720-2441

; TELEX: EZEKIEL

; INFORMATION FOR SEQ ID NO: 127:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 33 nucleotides

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-08-221-653-127

Query Match 100.0%; Score 24; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcaggcagt 24
|||||
DB 7 CTCGCAAGCACCCCTATCAGGAGT 30

RESULT 22

US-08-442-144A-127
; Sequence 127, Application US/08442144A
; Patent No. 6214583

; GENERAL INFORMATION:

; APPLICANT: Tai-An Cha

; APPLICANT: Eileen Beall

; APPLICANT: Bruce Irvine

; APPLICANT: Janice Kolberg

; APPLICANT: Michael S. Urdan

; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 148

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Chiron Corporation

; STREET: 4560 Horton Street

; CITY: Emeryville

; STATE: California

COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 Inch
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: Microsoft Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,144A
FILING DATE: MAY 16, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/221,653
FILING DATE: APRIL 1, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Doreen Yalco Trujillo
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CHIR-0121
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
TELEX:
INFORMATION FOR SEQ ID NO: 127:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 Nucleotides
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: DNA
US-08-442-144A-127

Query Match 100.0%; Score 24; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctcgcagcaccctatcagcagc 24
Db 7 CTCGCAGCACCTATCAGGCAGT 30

RESULT 23
US-08-441-970-127
Sequence 127 Application US/08441970
Patent No. 6297370
GENERAL INFORMATION:
APPLICANT: Tai-An Cha
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 Inch
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,970
FILING DATE: 16-MAY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/881,528
FILING DATE: 08-MAY-1992
APPLICATION NUMBER: 07/697,326
FILING DATE: 8 MAY 1991
ATTORNEY/AGENT INFORMATION:
NAME: Janluk, Anthony J.

REGISTRATION NUMBER: 29,809
REFERENCE/DOCKET NUMBER: C0772/7000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 720-3500
TELEFAX: (617) 720-2441
TELEX: EZEKIEL
INFORMATION FOR SEQ ID NO: 127:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-441-970-127

Query Match 100.0%; Score 24; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctcgcagcaccctatcagcagc 24
Db 7 CTCGCAGCACCTATCAGGCAGT 30

RESULT 24
US-08-429-181-16
Sequence 16 Application US/08429181
Patent No. 5635352
GENERAL INFORMATION:
APPLICANT: URDEA, MICHAEL S.
APPLICANT: FULTZ, TIMOTHY
APPLICANT: WARNER, BRIAN D.
APPLICANT: COLLINS, MARK
TITLE OF INVENTION: SOLUTION PHASE NUCLEIC ACID SANDWICH
TITLE OF INVENTION: ASSAYS HAVING REDUCED BACKGROUND NOISE
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: CITRON CORPORATION - INTELLECTUAL PROPERTY
STREET: 4560 HORTON STREET
CITY: EMERYVILLE
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,181
FILING DATE: 26-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,388
FILING DATE: 08-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: GOLDMAN, KENNETH M.
REGISTRATION NUMBER: 34,174
REFERENCE/DOCKET NUMBER: 0300,001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2719
TELEFAX: (510) 655-3542
TELEX: N/A
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 53 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-429-181-16

Query Match 100.0%; Score 24; DB 1; Length 53;
Best Local Similarity 100.0%; Pred. No. 3,4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagaccctatcagcagc 24
|||||
DB 27 CTCGCAAGCACCCTATCAGCAGT 50

RESULT 25
US-08-429-181-49
; Sequence 49, Application US/08429181
; Patent No. 5635352

; GENERAL INFORMATION:
; APPLICANT: URDEA, MICHAEL S.
; APPLICANT: FULTZ, TIMOTHY
; APPLICANT: WARNER, BRIAN D.
; APPLICANT: COLLINS, MARK
; TITLE OF INVENTION: SOLUTION PHASE NUCLEIC ACID SANDWICH
; TITLE OF INVENTION: ASSAYS HAVING REDUCED BACKGROUND NOISE
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION - INTELLECTUAL PROPERTY
; ADDRESS: R440
; STREET: 4560 HORTON STREET
; CITY: EMERYVILLE
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94608-2916

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/429,181
; FILING DATE: 26-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/164,388
; FILING DATE: 08-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDMAN, KENNETH M.
; REGISTRATION NUMBER: 34,174
; REFERENCE/DOCKET NUMBER: 0300.001
; TELEPHONE: (510) 601-2719
; TELEFAX: (510) 655-3542
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-429-181-49

Query Match 100.0%; Score 24; DB 1; Length 53;
Best Local Similarity 100.0%; Pred. No. 3,4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagaccctatcagcagc 24
|||||
DB 27 CTCGCAAGCACCCTATCAGCAGT 50

RESULT 26
US-08-164-388-16
; Sequence 16, Application US/08164388

; Patent No. 5681697
; GENERAL INFORMATION:
; APPLICANT: URDEA, MICHAEL S.
; APPLICANT: FULTZ, TIMOTHY
; APPLICANT: WARNER, BRIAN D.
; APPLICANT: COLLINS, MARK
; TITLE OF INVENTION: SOLUTION PHASE NUCLEIC ACID SANDWICH
; TITLE OF INVENTION: ASSAYS HAVING REDUCED BACKGROUND NOISE
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION - INTELLECTUAL PROPERTY
; ADDRESS: R440
; STREET: 4560 HORTON STREET
; CITY: EMERYVILLE
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94608-2916

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/164,388
; FILING DATE: 08-DEC-1993
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDMAN, KENNETH M.
; REGISTRATION NUMBER: 34,174
; REFERENCE/DOCKET NUMBER: 0300.001
; TELEPHONE: (510) 601-2719
; TELEFAX: (510) 655-3542
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-164-388-16

Query Match 100.0%; Score 24; DB 1; Length 53;
Best Local Similarity 100.0%; Pred. No. 3,4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagaccctatcagcagc 24
|||||
DB 27 CTCGCAAGCACCCTATCAGCAGT 50

RESULT 27
US-08-164-388-49
; Sequence 49, Application US/08164388
; Patent No. 5681697

; GENERAL INFORMATION:
; APPLICANT: URDEA, MICHAEL S.
; APPLICANT: FULTZ, TIMOTHY
; APPLICANT: WARNER, BRIAN D.
; APPLICANT: COLLINS, MARK
; TITLE OF INVENTION: SOLUTION PHASE NUCLEIC ACID SANDWICH
; TITLE OF INVENTION: ASSAYS HAVING REDUCED BACKGROUND NOISE
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION - INTELLECTUAL PROPERTY
; ADDRESS: R440
; STREET: 4560 HORTON STREET
; CITY: EMERYVILLE
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94608-2916

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.308
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,388
FILING DATE: 08-DEC-1993
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: GOLDMAN, KENNETH M.
REGISTRATION NUMBER: 34,174
REFERENCE/DOCKET NUMBER: 0300,001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2719
TELEFAX: (510) 655-3542
TELEX: N/A
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 53 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-164-388-49

Query Match 100.0%; Score 24; DB 1; Length 53;
Best Local Similarity 100.0%; Pred. No. 3,4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagaccctatcaggcagt 24
|||||
Db 27 CTCGCAAGCACCCTATCAGGAGT 50

RESULT 28
US-08-356-287-36/C
Sequence 36, Application US/08356287
Patent No. 5686272
GENERAL INFORMATION:
APPLICANT: Ronald L. Marshall
APPLICANT: John J. Carrino
APPLICANT: Joann Sustachek
TITLE OF INVENTION: AMPLIFICATION OF RNA SEQUENCES USING
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESS: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,287
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/891,543
FILING DATE: 29 MAY 1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul D. Yasger
REGISTRATION NUMBER: 37,477
REFERENCE/DOCKET NUMBER: 5172, US, P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-2341
TELEFAX: 708-938-2623

INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 57
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-356-287-36

Query Match 100.0%; Score 24; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 3,4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagaccctatcaggcagt 24
|||||
Db 57 CTCGCAAGCACCCTATCAGGAGT 34

RESULT 29
PCT-US93-04863-36/C
Sequence 36, Application PC/TUS9304863
GENERAL INFORMATION:
APPLICANT: Ronald L. Marshall
APPLICANT: John J. Carrino
APPLICANT: Joann C. Sustachek
TITLE OF INVENTION: AMPLIFICATION OF RNA SEQUENCES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESS: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04863
FILING DATE: 19930524
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/891,543
FILING DATE: 29 MAY 1992
ATTORNEY/AGENT INFORMATION:
NAME: Thomas D. Bralnard
REGISTRATION NUMBER: 32,459
REFERENCE/DOCKET NUMBER: 5172, PC, 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-4884
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 57
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
PCT-US93-04863-36

Query Match 100.0%; Score 24; DB 5; Length 57;
Best Local Similarity 100.0%; Pred. No. 3,4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagaccctatcaggcagt 24
|||||
Db 57 CTCGCAAGCACCCTATCAGGAGT 34

RESULT 30
US-08-429-181-31
Sequence 31, Application US/08429181
Patent No. 5635352
GENERAL INFORMATION:
APPLICANT: ORDEA, MICHAEL S.
APPLICANT: FULTZ, TIMOTHY
APPLICANT: WARNER, BRIAN D.
APPLICANT: COLLINS, MARK
TITLE OF INVENTION: SOLUTION PHASE NUCLEIC ACID SANDWICH
TITLE OF INVENTION: ASSAYS HAVING REDUCED BACKGROUND NOISE
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION - INTELLECTUAL PROPERTY
ADDRESS: R440
STREET: 4560 HORTON STREET
CITY: EMERYVILLE
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,181
FILING DATE: 26-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,388
FILING DATE: 08-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: GOLDMAN, KENNETH M.
REGISTRATION NUMBER: 34,174
REFERENCE/DOCKET NUMBER: 0300.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2719
TELEFAX: (510) 655-3542
TELEX: N/A
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-181-31

Query Match 100.0%; Score 24; DB 1; Length 64;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctgcgaagaccctatcaggcagt 24
|||||
DB 23 CTCGCAAGCACCCTATCAGGCGGT 46

RESULT 31
US-08-164-388-31
Sequence 31, Application US/08164388
Patent No. 5681697
GENERAL INFORMATION:
APPLICANT: ORDEA, MICHAEL S.
APPLICANT: FULTZ, TIMOTHY
APPLICANT: WARNER, BRIAN D.
APPLICANT: COLLINS, MARK
TITLE OF INVENTION: SOLUTION PHASE NUCLEIC ACID SANDWICH
TITLE OF INVENTION: ASSAYS HAVING REDUCED BACKGROUND NOISE
NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION - INTELLECTUAL PROPERTY
ADDRESS: R440
STREET: 4560 HORTON STREET
CITY: EMERYVILLE
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,388
FILING DATE: 08-DEC-1993
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: GOLDMAN, KENNETH M.
REGISTRATION NUMBER: 34,174
REFERENCE/DOCKET NUMBER: 0300.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2719
TELEFAX: (510) 655-3542
TELEX: N/A
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-164-388-31

Query Match 100.0%; Score 24; DB 1; Length 64;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctgcgaagaccctatcaggcagt 24
|||||
DB 23 CTCGCAAGCACCCTATCAGGCGGT 46

RESULT 32
US-08-356-287-25
Sequence 25, Application US/08356287
Patent No. 5686272
GENERAL INFORMATION:
APPLICANT: Ronald L. Marshall
APPLICANT: John J. Carriao
APPLICANT: Joann Sustachek
TITLE OF INVENTION: AMPLIFICATION OF RNA SEQUENCES USING
TITLE OF INVENTION: THE LIGASE CHAIN REACTION
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,287
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/891,543

FILING DATE: 29 MAY 1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul D. Yaeger
REGISTRATION NUMBER: 37,477
REFERENCE/DOCKET NUMBER: 5172.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-2341
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 23
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid (synthetic DNA)
US-08-356-287-25

Query Match 95.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 tcgcaagcacccatcagcagt 24
|||||
Db 1 TCGCAAGCACCTATCAGGCACT 23

RESULT 33
PCT-US93-04863-25

Sequence 25, Application PC/TUS9304863
GENERAL INFORMATION:
APPLICANT: Ronald L. Marshall
APPLICANT: John J. Carrino
APPLICANT: Joann C. Sustachek
TITLE OF INVENTION: ABBOTT LABORATORIES
TITLE OF INVENTION: AMPLIFICATION OF RNA SEQUENCES
TITLE OF INVENTION: USING THE LIGASE CHAIN REACTION
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESS: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04863
FILING DATE: 19930524
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/891,543
FILING DATE: 29 MAY 1992
ATTORNEY/AGENT INFORMATION:
NAME: Thomas D. Brainerd
REGISTRATION NUMBER: 32,459
REFERENCE/DOCKET NUMBER: 5172.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-4884
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 23
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid (synthetic DNA)
PCT-US93-04863-25

Query Match 95.8%; Score 23; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 tcgcaagcacccatcagcagt 24
|||||
Db 1 TCGCAAGCACCTATCAGGCACT 23

RESULT 34

US-08-240-547-20
Sequence 20, Application US/08240547
Patent No. 5527669
GENERAL INFORMATION:
APPLICANT: Resnick, Robert M.
APPLICANT: Young, Karen K.Y.
TITLE OF INVENTION: Primers and Probes for Detection of
TITLE OF INVENTION: Hepatitis C and No. 5527669el Variants
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESS: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: U.S.A.
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,547
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/918,844
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sias Ph.D., Stacey R.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-240-547-20

Query Match 95.8%; Score 23; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 tcgcaagcacccatcagcagt 24
|||||
Db 7 TCGCAAGCACCTATCAGGCACT 29

RESULT 35
US-08-356-287-27/c
Sequence 27, Application US/08356287
Patent No. 5686272
GENERAL INFORMATION:
APPLICANT: Ronald L. Marshall
APPLICANT: John J. Carrino
APPLICANT: Joann Sustachek

TITLE OF INVENTION: AMPLIFICATION OF RNA SEQUENCES USING
TITLE OF INVENTION: THE LIGASE CHAIN REACTION
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,287
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/891,543
FILING DATE: 29 MAY 1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul D. Yasger
REGISTRATION NUMBER: 37,477
REFERENCE/DOCKET NUMBER: 5172.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-2341
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 22
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid (synthetic DNA)
US-08-356-287-27

Query Match 91.7%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctgcgaagcaccctatcagca 22
|||||
Db 22 CTCGACAGCACCCTATCAGCA 1

RESULT 36
PCT-US93-04863-27/c
Sequence 27, Application PC/TUS9304863
GENERAL INFORMATION:
APPLICANT: Ronald L. Marshall
APPLICANT: John J. Carrino
APPLICANT: Joann C. Sustachek
TITLE OF INVENTION: AMPLIFICATION OF RNA SEQUENCES
TITLE OF INVENTION: USING THE LIGASE CHAIN REACTION
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04863

FILING DATE: 19930524
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/891,543
FILING DATE: 29 MAY 1992
ATTORNEY/AGENT INFORMATION:
NAME: Thomas D. Brainerd
REGISTRATION NUMBER: 32,459
REFERENCE/DOCKET NUMBER: 5172.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-4884
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 22
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid (synthetic DNA)
PCT-US93-04863-27

Query Match 91.7%; Score 22; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctgcgaagcaccctatcagca 22
|||||
Db 22 CTCGACAGCACCCTATCAGCA 1

RESULT 37
US-08-738-928-3
Sequence 3, Application US/08738928
Patent No. 5837442
GENERAL INFORMATION:
APPLICANT: Tsang, Sue Y.
TITLE OF INVENTION: Oligonucleotide Primers for Amplifying
TITLE OF INVENTION: HCV Nucleic Acid
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,928
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 9263
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-738-928-3

Query Match 87.5%; Score 21; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 gcaagcaccctatcaggcagt 24
|||||
Db 1 gcaagcaccctatcaggcagt 21

RESULT 38

US-08-738-928-2
Sequence 2, Application US/08738928
Patent No. 5837442

GENERAL INFORMATION:
APPLICANT: Tsang, Sue Y.
TITLE OF INVENTION: Oligonucleotide Primers for Amplifying
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: U.S.A.
ZIP: 07110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,928
FILING DATE:
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 9263
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-738-928-2

Query Match 87.5%; Score 21; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 gcaagcaccctatcaggcagt 24
|||||
Db 1 gcaagcaccctatcaggcagt 21

RESULT 39

US-09-039-866-4
Sequence 4, Application US/09039866
Patent No. 6001611

GENERAL INFORMATION:
APPLICANT: Will, Stephen G.
TITLE OF INVENTION: MODIFIED NUCLEIC ACID AMPLIFICATION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Roche Molecular Systems
STREET: 1080 U.S. Highway 202
CITY: Branchburg

STATE: New Jersey
COUNTRY: United States
ZIP: 08876

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,866
FILING DATE:
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 1023P
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-039-866-4

Query Match 87.5%; Score 21; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 gcaagcaccctatcaggcagt 24
|||||
Db 1 gcaagcaccctatcaggcagt 21

RESULT 40

US-08-474-700B-35/C
Sequence 35, Application US/08474700B
Patent No. 6001990

GENERAL INFORMATION:
APPLICANT: Wands, Jack
APPLICANT: Wakita, Takaji
TITLE OF INVENTION: MORAPOUR, Darius
TITLE OF INVENTION: ANTISENSE INHIBITION OF HEPATITIS C
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,700B
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,382
FILING DATE: 10 May 1994
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/279001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-474-700B-35

Job time: 5905 sec

Query Match 87.5%; Score 21; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagaccctatacaggc 21
|||||
Db 21 CTCGCAAGCACCTATCAGGC 1

RESULT 41
PCT-US95-05812-35/c
Sequence 35, Application PC/TUS9505812
GENERAL INFORMATION:
APPLICANT: Wakita, Takaji
APPLICANT: Wands, Jack
TITLE OF INVENTION: ANTISENSE INHIBITION OF
TITLE OF INVENTION: HEPATITIS C VIRUS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
City: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05812
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,382
FILING DATE: 10 May 1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/221001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SRO ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-05812-35

Query Match 87.5%; Score 21; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagaccctatacaggc 21
|||||
Db 21 CTCGCAAGCACCTATCAGGC 1

Search completed: August 26, 2002, 22:17:12

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 22:14:58 ; Search time 323.25 Seconds
(without alignments)
100.186 Million cell updates/sec

Title: US-10-037-990A-2
Perfect score: 24
Sequence: 1 ctcgaagcacccatcagcagcagt 24

Scoring table: OLIGO_NDC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 21

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
No matches found				

Search completed: August 26, 2002, 22:14:58
Job time: 9022 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 21:20:52 ; Search time 1915.63 seconds
(without alignments)
262.178 Million cell updates/sec

Title: US-10-037-990A-2

Perfect score: 24

Sequence: 1 ctcgaagcaccctatcagcagc 24

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 21

Total number of hits satisfying chosen parameters: 54

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database :

GenEmbl: 1: gb_da:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlg_inv:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
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1	c	24	100.0	24	6	A68286	A68286 Sequence 7
2	c	24	100.0	24	6	AR011642	AR011642 Sequence
3	3	24	100.0	24	6	AR054579	AR054579 Sequence
4	4	24	100.0	24	6	AX003942	AX003942 Sequence
5	5	24	100.0	24	6	AX021564	AX021564 Sequence
6	6	24	100.0	24	6	AX021623	AX021623 Sequence
7	c	24	100.0	24	6	AX040437	AX040437 Sequence
8	7	24	100.0	24	6	AX147012	AX147012 Sequence
9	9	24	100.0	24	6	I22159	I22159 Sequence 18
10	10	24	100.0	24	6	I26948	I26948 Sequence 16
11	11	24	100.0	24	6	I40300	I40300 Sequence 8
12	12	24	100.0	24	6	I59677	I59677 Sequence 8
13	13	24	100.0	24	6	I68635	I68635 Sequence 8
14	14	24	100.0	24	6	A39032	A39032 Sequence 4
15	15	24	100.0	24	6	AR063366	AR063366 Sequence
16	16	24	100.0	24	6	AR123557	AR123557 Sequence
17	17	24	100.0	24	6	AX023094	AX023094 Sequence
18	18	24	100.0	24	6	E50770	E50770 Vector expr
19	19	24	100.0	24	6	I22160	I22160 Sequence 19
20	20	24	100.0	24	6	AX202931	AX202931 Sequence
21	21	24	100.0	24	6	AX202933	AX202933 Sequence
22	c	24	100.0	24	6	AX282438	AX282438 Sequence
23	23	24	100.0	24	6	BD000268	BD000268 Oligonuc1
24	24	24	100.0	24	6	AR094974	AR094974 Sequence
25	25	24	100.0	24	6	AR004397	AR004397 Sequence
26	26	24	100.0	24	6	AR064936	AR064936 Sequence
27	27	24	100.0	24	6	AR097189	AR097189 Sequence
28	28	24	100.0	24	6	AR130687	AR130687 Sequence
29	29	24	100.0	24	6	AR172036	AR172036 Sequence
30	30	24	100.0	24	6	I82872	I82872 Sequence 51
31	31	24	100.0	24	6	E17189	E17189 Partial seq
32	c	24	100.0	24	6	AX284180	AX284180 Sequence
33	33	24	100.0	24	6	I44587	I44587 Sequence 16
34	34	24	100.0	24	6	I44620	I44620 Sequence 49
35	35	24	100.0	24	6	I70992	I70992 Sequence 16
36	36	24	100.0	24	6	I71025	I71025 Sequence 49
37	c	24	100.0	24	6	I73305	I73305 Sequence 36
38	c	24	100.0	24	6	AX003948	AX003948 Sequence
39	c	24	100.0	24	6	AX021624	AX021624 Sequence
40	40	24	100.0	24	6	I44602	I44602 Sequence 31
41	41	24	100.0	24	6	I71007	I71007 Sequence 31
42	c	24	100.0	24	6	AX021668	AX021668 Sequence
43	43	23	95.8	23	6	I73294	I73294 Sequence 25
44	44	23	95.8	23	6	I22161	I22161 Sequence 20
45	c	22	91.7	22	6	I73296	I73296 Sequence 27
46	46	22	91.7	22	6	AX250665	AX250665 Sequence
47	47	21	87.5	25	6	AX250673	AX250673 Sequence
48	48	21	87.5	27	6	AR054577	AR054577 Sequence
49	49	21	87.5	27	6	BD000267	BD000267 Oligonuc1
50	50	21	87.5	28	6	AR054576	AR054576 Sequence
51	51	21	87.5	28	6	AR094138	AR094138 Sequence
52	c	21	87.5	28	6	AR094997	AR094997 Sequence
53	53	21	87.5	28	6	AX147022	AX147022 Sequence
54	54	21	87.5	46	6	E58845	E58845 Method for

ALIGNMENTS

RESULT	1	A68286	Sequence 7 from Patent WO9746716.	24 bp	DNA	linear	PAT 06-MAY-1999
LOCUS	A68286						
DEFINITION	A68286						
ACCESSION	A68286						
VERSION	A68286.1	GI:4759407					
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE	1	(bases 1 to 24)					
AUTHORS	Bosio, P., Strumia, C. and Clemenza, F.						
TITLE	METHOD TO DETECT HCV SPECIFIC NUCLEIC ACIDS						
JOURNAL	Patent: WO 9746716-A 7 11-DEC-1997;						

WABCO B V (NL)
Other Publication IT RM960404 19971209.
COMMENT Location/Qualifiers
FEATURES 1. 24
source /organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 6 a 9 c 5 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctgcgaagcaccctatcagcagc 24
|||||
Db 1 CTCGCAAGCACCCCTATCAGCAGT 24

RESULT 2
LOCUS AR011642 24 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 51 from patent US 5763159.
ACCESSION AR011642
VERSION AR011642.1 GI:3969632
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Slimmons, P., Char, S.-W. and Yap, P. Lee.
TITLE Hepatitis-C virus testing
JOURNAL Patent: US 5763159-A 51 09-JUN-1998;
FEATURES Location/Qualifiers
source 1. 24
/organism="unknown"
BASE COUNT 4 a 5 c 9 g 6 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctgcgaagcaccctatcagcagc 24
|||||
Db 24 CTCGCAAGCACCCCTATCAGCAGT 1

RESULT 3
LOCUS AR054579 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5837442.
ACCESSION AR054579
VERSION AR054579.1 GI:5980156
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Tsang, S. Yen.
TITLE Oligonucleotide primers for amplifying HCV nucleic acid
JOURNAL Patent: US 5837442-A 5 17-NOV-1998;
FEATURES Location/Qualifiers
source 1. 24
/organism="unknown"
BASE COUNT 6 a 9 c 5 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctgcgaagcaccctatcagcagc 24
|||||
Db 1 CTCGCAAGCACCCCTATCAGCAGT 24

RESULT 4
LOCUS AX003942 24 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 2 from Patent WO9923249.
ACCESSION AX003942
VERSION AX003942.1 GI:9927602
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 24)
AUTHORS Kessler, C. and Bartl, K.
TITLE Specific and sensitive method for detecting nucleic acids
JOURNAL Patent: WO 9923249-A 2 14-MAY-1999;
FEATURES KESSLER CHRISTOPH (DE); BARTL KNUF (DE)
source 1. 24
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="KY78"
BASE COUNT 6 a 9 c 5 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctgcgaagcaccctatcagcagc 24
|||||
Db 1 CTCGCAAGCACCCCTATCAGCAGT 24

RESULT 5
LOCUS AX021564 24 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 2 from Patent WO9924606.
ACCESSION AX021564
VERSION AX021564.1 GI:10044848
KEYWORDS
SOURCE Hepatitis C virus.
ORGANISM Hepatitis C virus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Kessler, C., Bartl, K., Habershausen, G. and Orum, H.
TITLE Specific and sensitive nucleic acid detection method
JOURNAL Patent: WO 9924606-A 2 20-MAY-1999;
FEATURES KESSLER CHRISTOPH (DE); BARTL KNUF (DE); HABERHAUSEN GERD (DE);
source 1. 24
Location/Qualifiers
/organism="Hepatitis C virus"
/db_xref="taxon:11103"
BASE COUNT 6 a 9 c 5 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctgcgaagcaccctatcagcagc 24
|||||
Db 1 CTCGCAAGCACCCCTATCAGCAGT 24

RESULT 6
LOCUS AX021623 24 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 2 from Patent WO9923250.
ACCESSION AX021623
VERSION AX021623.1 GI:10044906
KEYWORDS Hepatitis C virus.
SOURCE Hepatitis C virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Kessler,C., Bartl,K., Haberkhausen,G. and Orum,H.
TITLE Specific and sensitive method for detecting nucleic acids
JOURNAL Patent: WO 9923250-A 2 14-MAY-1999;
KESLER CHRISTOPH (DE); BARTL KNUF (DE); HABERHAUSEN GERD (DE);
ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES
source 1..24
Location/Qualifiers
/organism="Hepatitis C virus"
/db_xref="taxon:11103"
BASE COUNT 6 a 9 c 5 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctcgaagcaccctatcagcagt 24
|||||
Db 1 CTCGCAAGCACCTATCAGGCACT 24

RESULT 7
LOCUS AX040437 24 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 2 from Patent WO0063444.
ACCESSION AX040437
VERSION AX040437.1 GI:11230244
KEYWORDS Hepatitis C virus.
SOURCE Hepatitis C virus.
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Budkowska,A., Mailard,P., Nitkiewicz,J. and Crainic,R.
TITLE Method for detecting hepatitis C virus with hydridomas
JOURNAL Patent: WO 0063444-A 2 26-OCT-2000;
INSTITUT PASTEUR (FR)
FEATURES
source 1..24
Location/Qualifiers
/organism="Hepatitis C virus"
/db_xref="taxon:11103"
BASE COUNT 4 a 5 c 9 g 6 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctcgaagcaccctatcagcagt 24
|||||
Db 24 CTCGCAAGCACCTATCAGGCACT 1

RESULT 8
LOCUS AX147012 24 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 6 from Patent WO0137291.
ACCESSION AX147012
VERSION AX147012.1 GI:14346283

KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 24)
AUTHORS Weindel,K., Riedling,M. and Geiger,A.
TITLE Magnetic glass particles, method for their preparation and uses
JOURNAL Patent: WO 0137291-A 6 25-MAY-2001;
Roche Diagnostics GmbH (DE)
FEATURES
source 1..24
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
misc_feature 1
/note="Synthetic oligonucleotide primer (HCV reverse)"
BASE COUNT 6 a 9 c 5 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctcgaagcaccctatcagcagt 24
|||||
Db 1 CTCGCAAGCACCTATCAGGCACT 24

RESULT 9
LOCUS I22159 24 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 18 from patent US 5527669.
ACCESSION I22159
VERSION I22159.1 GI:1602513
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Resnick,R.M. and Young,K.K.Y.
TITLE Methods, primers and probes for detection of hepatitis C and novel variants
JOURNAL Patent: US 5527669-A 18 18-JUN-1996;
Location/Qualifiers
FEATURES
source 1..24
Location/Qualifiers
/organism="unknown"
BASE COUNT 6 a 9 c 5 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctcgaagcaccctatcagcagt 24
|||||
Db 1 CTCGCAAGCACCTATCAGGCACT 24

RESULT 10
LOCUS I26948 24 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 16 from patent US 5561058.
ACCESSION I26948
VERSION I26948.1 GI:1606818
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gelfand,D.H., Myers,T.W. and Sigua,C.L.

TITLE Methods for coupled high temperatures reverse transcription and
polymerase chain reactions
JOURNAL Patent: US 5561058-A 16 01-OCT-1996;
FEATURES Location/Qualifiers
source 1..24
BASE COUNT 6 a 9 c 5 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctcgaagcacccctatcaggcagt 24
Db 1 CTCGCAAGCACCCCTATCAGGCACT 24

RESULT 11
LOCUS I40300 24 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 8 from patent US 5620852.
ACCESSION I40300
VERSION I40300.1 GI:2082592
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Lin, L., Cimino, G. and Zhu, Y.S.
TITLE Nucleic acid preparation methods
JOURNAL Patent: US 5620852-A 8 15-APR-1997;
FEATURES Location/Qualifiers
source 1..24
BASE COUNT 6 a 9 c 5 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctcgaagcacccctatcaggcagt 24
Db 1 CTCGCAAGCACCCCTATCAGGCACT 24

RESULT 12
LOCUS I59677 24 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 8 from patent US 5654179.
ACCESSION I59677
VERSION I59677.1 GI:2478309
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Lin, L.
TITLE Nucleic acid preparation methods
JOURNAL Patent: US 5654179-A 8 05-AUG-1997;
FEATURES Location/Qualifiers
source 1..24
BASE COUNT 6 a 9 c 5 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctcgaagcacccctatcaggcagt 24
Db 1 CTCGCAAGCACCCCTATCAGGCACT 24

Qy 1 ctcgaagcacccctatcaggcagt 24
Db 1 CTCGCAAGCACCCCTATCAGGCACT 24

RESULT 13
LOCUS I68635 24 bp DNA linear PAT 04-FEB-1998
DEFINITION Sequence 8 from patent US 5677124.
ACCESSION I68635
VERSION I68635.1 GI:2830757
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dubois, D.B., Winkler, M.M. and Pasloske, B.L.
TITLE Ribonuclease resistant viral RNA standards
JOURNAL Patent: US 5677124-A 8 14-OCT-1997;
FEATURES Location/Qualifiers
source 1..24
BASE COUNT 6 a 9 c 5 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctcgaagcacccctatcaggcagt 24
Db 1 CTCGCAAGCACCCCTATCAGGCACT 24

RESULT 14
LOCUS A39032 26 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 4 from Patent WO9412670.
ACCESSION A39032
VERSION A39032.1 GI:2295418
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Maertens, G., Stuyver, L., Rossau, R. and Van, H.H.
TITLE PROCESS FOR TYPING OF HCV ISOLATES
JOURNAL Patent: WO 9412670-A 4 09-JUN-1994;
COMMENT INNOGENETICS NV (BE)
Other publication AU 5628294 940622
Other publication CA 2128528 940609
Other publication JP 7503143T 950406.
FEATURES Location/Qualifiers
source 1..26
BASE COUNT 7 a 10 c 5 g 4 t
ORIGIN /db_xref="taxon:32644"

Query Match 100.0%; Score 24; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctcgaagcacccctatcaggcagt 24
Db 3 CTCGCAAGCACCCCTATCAGGCACT 26

RESULT 15
AR063366

LOCUS AR063366 26 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5846704.
ACCESSION AR063366
VERSION AR063366.1 GI:5992674
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.
TITLE Process for typing of HCV isolates
JOURNAL Patent: US 5846704-A 4 08-DEC-1998;
FEATURES Location/Qualifiers
source 1..26
BASE COUNT 7 a 10 c 5 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcagcagc 24
|||||
DB 3 CTCGCAAGCACCCTATCAGCAGT 26

RESULT 16
AR123557
LOCUS AR123557 26 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 4 from patent US 6171784.
ACCESSION AR123557
VERSION AR123557.1 GI:14108918
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.
TITLE Process for typing of HCV isolates
JOURNAL Patent: US 6171784-A 4 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..26
BASE COUNT 7 a 10 c 5 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcagcagc 24
|||||
DB 3 CTCGCAAGCACCCTATCAGCAGT 26

RESULT 17
AX023094
LOCUS AX023094 26 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 4 from Patent EP0905258.
ACCESSION AX023094
VERSION AX023094.1 GI:10046559
KEYWORDS
SOURCE Hepatitis C virus.
ORGANISM Hepatitis C virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
REFERENCE 1 (bases 1 to 26)
AUTHORS
TITLE Method for detecting nucleic acid sequences based on the use of solid phase immobilised nucleotide probes (line probe assay)

JOURNAL Patent: EP 0905258-A 4 31-MAR-1999;
INNOGENETICS NV (BE)
FEATURES Location/Qualifiers
source 1..26
/organism="Hepatitis C virus"
/isolate="HCV"
/db_xref="taxon:11103"
/map="POSITION -29 OF 5' END"
misc-feature 1..26
BASE COUNT 7 a 10 c 5 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcagcagc 24
|||||
DB 3 CTCGCAAGCACCCTATCAGCAGT 26

RESULT 18
E50770
LOCUS E50770 26 bp DNA linear PAT 31-JAN-2002
DEFINITION Vector expressing full-length gene of RNA virus and utilization thereof.
ACCESSION E50770
VERSION E50770.1 GI:18628195
KEYWORDS JP 2000152793-A/23.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 26)
AUTHORS Obara,M., Obara,K., Tabira,K., Matsuzaki,J. and Om,H.
TITLE Vector expressing full-length gene of RNA virus and utilization
JOURNAL Patent: JP 2000152793-A 23 06-JUN-2000;
TOKYO METROPOLITAN ORGANIZATION FOR MEDICAL RESEARCH, CHUGAI PHARMACEUT CO LTD
COMMENT OS Artificial Sequence
PN JP 2000152793-A/23
PD 06-JUN-2000
PF 24-JUN-1999 JP 1999178347
PR
PI MICHIKORI OBARA, KYOKO OBARA, KAZUNARI TABIRA, JUNICHI MATSUZAKI,
PI HIROSHI OMORI
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/70,C12N15/00,C12N5/00 CC

FEATURES
source 1..26
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 7 a 10 c 5 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcagcagc 24
|||||
DB 3 CTCGCAAGCACCCTATCAGCAGT 26

RESULT 19
I22160
LOCUS I22160 26 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 19 from patent US 5527669.

ACCESSION 122160 GI:1602514
VERSION 122160.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
REFERENCE 1 (bases 1 to 26)
AUTHORS Resnick,R.M. and Young,R.K.Y.
TITLE Methods, primers and probes for detection of hepatitis C and novel variants
JOURNAL Patent: US 5527669-A 19 18-JUN-1996;
FEATURES
source
1. .26
Location/Qualifiers
BASE COUNT 7 a 10 c 5 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcaggcagt 24
|||||
Db 3 ctgcgaagcaccctatcaggcagt 26

RESULT 20
AX202931 27 bp DNA linear PAT 30-AUG-2001
LOCUS AX202931
DEFINITION Sequence 6 from Patent WO0152612.
ACCESSION AX202931
VERSION AX202931.1 GI:15392394
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Elaissari,A., Mandrand,B., Delair,T., Spencer,D. and Arkis,A.
TITLE Method for isolating proteins or protein and nucleic acid associations, or particle and protein complexes, reagent and uses
JOURNAL Patent: WO 0152612-A 6 26-JUL-2001;
FEATURES
source
1. .27
Location/Qualifiers
BASE COUNT 8 a 10 c 5 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcaggcagt 24
|||||
Db 2 ctgcgaagcaccctatcaggcagt 25

RESULT 21
AX202933 27 bp DNA linear PAT 30-AUG-2001
LOCUS AX202933
DEFINITION Sequence 8 from Patent WO0152612.
ACCESSION AX202933
VERSION AX202933.1 GI:15392396
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Elaissari,A., Mandrand,B., Delair,T., Spencer,D. and Arkis,A.

TITLE Method for isolating proteins or protein and nucleic acid associations, or particle and protein complexes, reagent and uses
JOURNAL Patent: WO 0152612-A 8 26-JUL-2001;
BIO MERIEUX (FR)
FEATURES
source
1. .27
Location/Qualifiers
BASE COUNT 8 a 10 c 5 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcaggcagt 24
|||||
Db 2 ctgcgaagcaccctatcaggcagt 25

RESULT 22
AX282438 27 bp mRNA linear PAT 02-NOV-2001
LOCUS AX282438/C
DEFINITION Sequence 10 from Patent WO0166721.
ACCESSION AX282438
VERSION AX282438.1 GI:16609569
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (sites)
AUTHORS Usman,N., Mcswigen,J.A., Zinnen,S., Selwert,S., Haerberli,P., Chowrita,B. and Blatt,L.
TITLE Nucleic acid sensor molecules
JOURNAL Patent: WO 0166721-A 10 13-SEP-2001;
FEATURES
source
1. .27
Location/Qualifiers
BASE COUNT 4 a 5 c 10 g 8 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcaggcagt 24
|||||
Db 25 ctgcgaagcaccctatcaggcagt 2

RESULT 23
BD000268 27 bp DNA linear PAT 31-JAN-2002
LOCUS BD000268
DEFINITION Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof.
ACCESSION BD000268
VERSION BD000268.1 GI:18623347
KEYWORDS JP 2000279200-A/6.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 27)
AUTHORS Lynen,J.M. and Gorman,K.M.
TITLE Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof
JOURNAL Patent: JP 2000279200-A 6 10-OCT-2000;
ORTHOD CLINICAL DIAGNOSTICS INC

COMMENT OS Artificial Sequence
PN JP 2000279200-A/6
PD 10-OCT-2000
PF 03-FEB-2000 JP 2000032656
PR 03-FEB-1999 US 60/118497
PI JEFFREY M LYNN, KEVIN M GORMAN
PC C1201/68, C12N15/09, C12N15/09, C12R1/92, C12N15/00, C12N15/00,
PC C12R1/92)
CC
FH Key Location/Qualifiers
FT source 1..27 /organism='Artificial Sequence',
source 1..27 /organism='synthetic construct'
/db_xref='taxon:32630'
BASE COUNT 8 a 10 c 5 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctcgcaagcacccctatcagcagt 24
|||||
DB 3 CTCGCAAGCACCCCTATCAGCAGCT 26

RESULT 24
AR094974 AR094974 28 bp DNA linear PAT 08-SEP-2000
LOCUS
DEFINITION Sequence 12 from patent US 6001990.
ACCESSION AR094974
VERSION AR094974.1 GI:10022401
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Wands, J.R., Wakita, T. and Moradpour, D.
TITLE Antisense inhibition of hepatitis C virus
JOURNAL Patent: US 6001990-A 12 14-DEC-1999;
FEATURES Location/Qualifiers
source 1..28
BASE COUNT 8 a 11 c 5 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctcgcaagcacccctatcagcagt 24
|||||
DB 2 CTCGCAAGCACCCCTATCAGCAGCT 25

RESULT 25
AR004397 AR004397 33 bp DNA linear PAT 04-DEC-1998
LOCUS
DEFINITION Sequence 51 from patent US 5747244.
ACCESSION AR004397
VERSION AR004397.1 GI:3965276
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Sheridan, P., Chang, C.-A., Running, J. and Urdea, M.S.
TITLE Nucleic acid probes immobilized on polystyrene surfaces
JOURNAL Patent: US 5747244-A 51 05-MAY-1998;

FEATURES Location/Qualifiers
source 1..33 /organism="unknown"
BASE COUNT 8 a 12 c 9 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctcgcaagcacccctatcagcagt 24
|||||
DB 7 CTCGCAAGCACCCCTATCAGCAGCT 30

RESULT 26
AR064936 AR064936 33 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 61 from patent US 5849481.
ACCESSION AR064936
VERSION AR064936.1 GI:5995152
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Urdea, M.S., Horn, T., Chang, C.-A., Warner, B. and Fultz, T.J.
TITLE Nucleic acid hybridization assays employing large comb-type
JOURNAL branched polynucleotides
FEATURES Patent: US 5849481-A 61 15-DEC-1998;
source 1..33 Location/Qualifiers
BASE COUNT 8 a 12 c 9 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctcgcaagcacccctatcagcagt 24
|||||
DB 7 CTCGCAAGCACCCCTATCAGCAGCT 30

RESULT 27
AR097189 AR097189 33 bp DNA linear PAT 14-FEB-2001
LOCUS
DEFINITION Sequence 127 from patent US 6071693.
ACCESSION AR097189
VERSION AR097189.1 GI:12805919
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Cha, T., Beall, E., Irvine, B., Kolberg, J. and Urdea, M.S.
TITLE HCV genomic sequences for diagnostics and therapeutics
JOURNAL Patent: US 6071693-A 127 06-JUN-2000;
FEATURES Location/Qualifiers
source 1..33
BASE COUNT 8 a 12 c 9 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctcgcaagcacccctatcagcagt 24

Db 7 CTCGCAAGCACCTATCAGGCACT 30
|||||
RESULT 28
ARI30687
LOCUS ARI30687 33 bp DNA
DEFINITION Sequence 127 from patent US 6190864.
ACCESSION ARI30687
VERSION ARI30687.1 GI:14119012
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Cha,T., Beall,E., Irvine,B., Kolberg,J. and Urdea,M.S.
TITLE HCV genomic sequences for diagnostics and therapeutics
JOURNAL Patent: US 6190864-A 127 20-FEB-2001;
FEATURES
Location/Qualifiers
1..33
/organism="unknown"
BASE COUNT 8 a 12 c 9 g 4 t
ORIGIN
Query Match 100.0%; Score 24; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ctgcgaagcacctatcaggcagt 24
|||||
Db 7 CTCGCAAGCACCTATCAGGCACT 30
RESULT 29
ARI172036
LOCUS ARI172036 33 bp DNA
DEFINITION Sequence 127 from patent US 6297370.
ACCESSION ARI172036
VERSION ARI172036.1 GI:17910986
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Cha,T., A., Beall,E., Irvine,B., Kolberg,J. and Urdea,M.S.
TITLE HCV genomic sequences for diagnostics and therapeutics
JOURNAL Patent: US 6297370-A 127 02-OCT-2001;
FEATURES
Location/Qualifiers
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/organism="unknown"
BASE COUNT 8 a 12 c 9 g 4 t
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Best Local Similarity 100.0%; Pred. No. 0.00032;
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Db 7 CTCGCAAGCACCTATCAGGCACT 30
RESULT 30
I82872
LOCUS I82872 33 bp DNA
DEFINITION Sequence 51 from patent US 5712383.
ACCESSION I82872
VERSION I82872.1 GI:3211169
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 33)
AUTHORS Sheridan,P., Chang,C.-A., Running,J. and Urdea,M.S.
TITLE Process for immobilizing nucleic acid probes on polystyrene
JOURNAL Patent: US 5712383-A 51 27-JAN-1998;
FEATURES
Location/Qualifiers
1..33
/organism="unknown"
BASE COUNT 8 a 12 c 9 g 4 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ctgcgaagcacctatcaggcagt 24
|||||
Db 7 CTCGCAAGCACCTATCAGGCACT 30
RESULT 31
E17189
LOCUS E17189 40 bp DNA
DEFINITION Partial sequence of HCV gene.
ACCESSION E17189
VERSION E17189.1 GI:5711872
KEYWORDS JP 1998248579-A/3.
SOURCE Hepatitis C virus.
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepadnavirus.
REFERENCE 1 (bases 1 to 40)
AUTHORS Obara,M., Inoue,K., Katsume,A., Takeuchi,T. and Kawaguchi,R.
TITLE MEASUREMENT OF HCV GENE BY REAL TIME DETECTION PCR METHOD, AND
PRIMER AND PROBE TO BE USED THEREFOR
JOURNAL Patent: JP 1998248579-A 3 22-SEP-1998;
COMMENT TOKYO MET GOV RINSHIYOU IGAKU SOGO KENKYUSHO, S R L:KK
OS Hepatitis C virus
PN JP 1998248579-A/3
PD 22-SEP-1998
PF 05-MAR-1997 JP 1997067321
PI OBARA MICHINORI, INOUE KAZUAKI, KATSUME ASANO, TAKEUCHI TOMOKO,
PI KAWAGUCHI RYUJI
PC C12N15/09,C07H21/02,C07H21/04,C12Q1/68,G01N33/566,G01N33/576;
CC CC strandedness: Double;
CC topology: Linear;
FH Key
FH Location/Qualifiers
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Location/Qualifiers
1..40
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BASE COUNT 9 a 17 c 9 g 5 t
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Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 13 CTCGCAAGCACCTATCAGGCACT 36
RESULT 32
AX284180
LOCUS AX284180/c 47 bp DNA
DEFINITION Sequence 1 from Patent WO0179420.

ACCESSION AX284180
VERSION AX284180.1 GI:17044868
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (sites)
AUTHORS Faruqi,A.F.
TITLE Detection and amplification or rna using target-mediated ligation
JOURNAL Patent: WO 01/9420-A 1 25-OCT-2001;
FEATURES MOLECULAR STAGING, INC. (US)
source Location/Qualifiers
1..47
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic Target"
BASE COUNT 7 a 11 c 18 g 11 t
ORIGIN

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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 33

LOCUS I44587 53 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 16 from patent US 5635352.
ACCESSION I44587
VERSION I44587.1 GI:2469300
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 53)
AUTHORS Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
TITLE Solution phase nucleic acid sandwich assays having reduced background noise
JOURNAL Patent: US 5635352-A 16 03-JUN-1997;
FEATURES Location/Qualifiers
source 1..53
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BASE COUNT 12 a 17 c 15 g 9 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 53;
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JOURNAL
FEATURES
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BASE COUNT 12 a 17 c 15 g 9 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctgcgaagcaccctatcagcagt 24
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Db 27 CTCGCAAGCACCTATCAGGCACT 50

RESULT 34
LOCUS I44620 53 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 49 from patent US 5635352.
ACCESSION I44620
VERSION I44620.1 GI:2469333
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 53)
AUTHORS Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.

TITLE Solution phase nucleic acid sandwich assays having reduced background noise
JOURNAL Patent: US 5635352-A 49 03-JUN-1997;
FEATURES Location/Qualifiers
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BASE COUNT 12 a 17 c 15 g 9 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 53;
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctgcgaagcaccctatcagcagt 24
|||||
Db 27 CTCGCAAGCACCTATCAGGCACT 50

RESULT 35

LOCUS I70992 53 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 16 from patent US 5681697.
ACCESSION I70992
VERSION I70992.1 GI:3007127
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 53)
AUTHORS Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
TITLE Solution phase nucleic acid sandwich assays having reduced background noise and kits therefor
JOURNAL Patent: US 5681697-A 16 28-OCT-1997;
FEATURES Location/Qualifiers
source 1..53
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BASE COUNT 12 a 17 c 15 g 9 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctgcgaagcaccctatcagcagt 24
|||||
Db 27 CTCGCAAGCACCTATCAGGCACT 50

RESULT 36
LOCUS I71025 53 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 49 from patent US 5681697.
ACCESSION I71025
VERSION I71025.1 GI:3007160
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 53)
AUTHORS Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
TITLE Solution phase nucleic acid sandwich assays having reduced background noise and kits therefor
JOURNAL Patent: US 5681697-A 49 28-OCT-1997;
FEATURES Location/Qualifiers
source 1..53
/organism="unknown"
BASE COUNT 12 a 17 c 15 g 9 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctgcgaagcaccctatcagcagt 24
|||||
Db 27 CTCGCAAGCACCTATCAGGCACT 50

RESULT 36
LOCUS I71025 53 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 49 from patent US 5681697.
ACCESSION I71025
VERSION I71025.1 GI:3007160
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 53)
AUTHORS Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
TITLE Solution phase nucleic acid sandwich assays having reduced background noise and kits therefor
JOURNAL Patent: US 5681697-A 49 28-OCT-1997;
FEATURES Location/Qualifiers
source 1..53
/organism="unknown"
BASE COUNT 12 a 17 c 15 g 9 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 53;

Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ctgcgaagcaccctatcagcagt 24
|||||
Db 27 CTGCGAAGCACCCTATCAGCAGT 50

RESULT 37
LOCUS I73305 57 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 36 from patent US 5686272.
ACCESSION I73305
VERSION I73305.1 GI:3009444
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 57)
AUTHORS Marshall,R.L., Carrino,J.J. and Sustachek,J.C.
TITLE Amplification of RNA sequences using the ligase chain reaction
JOURNAL Patent: US 5686272-A 36 11-NOV-1997;
FEATURES
source 1..57
/organism="unknown"
BASE COUNT 9 a 9 c 23 g 16 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctgcgaagcaccctatcagcagt 24
|||||
Db 57 CTGCGAAGCACCCTATCAGCAGT 34

RESULT 38
LOCUS AX003948 59 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 8 from Patent WO923249.
ACCESSION AX003948
VERSION AX003948.1 GI:9927608
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 59)
AUTHORS Kessler,C. and Bartl,K.
TITLE Specific and sensitive method for detecting nucleic acids
JOURNAL Patent: WO 9923249-A 8 14-MAY-1999;
KESSELER CHRISTOPH (DE); BARTL KNUF (DE)
FEATURES
source 1..59
/organism="Hepatitis C virus"
/db_xref="taxon:11103"
BASE COUNT 9 a 16 c 21 g 13 t
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 26 CTGCGAAGCACCCTATCAGCAGT 3

RESULT 39
AX021624/c
Unclassified.

LOCUS AX021624 59 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 3 from Patent WO9923250.
ACCESSION AX021624
VERSION AX021624.1 GI:10044907
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 59)
AUTHORS Kessler,C., Bartl,K., Haberland,H., G. and Orum,H.
TITLE Specific and sensitive method for detecting nucleic acids
JOURNAL Patent: WO 9923250-A 3 14-MAY-1999;
KESSELER CHRISTOPH (DE); BARTL KNUF (DE); HABERHAUSEN GERD (DE);
ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES
source 1..59
/organism="Hepatitis C virus"
/db_xref="taxon:11103"
BASE COUNT 9 a 16 c 21 g 13 t
ORIGIN

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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctgcgaagcaccctatcagcagt 24
|||||
Db 26 CTGCGAAGCACCCTATCAGCAGT 3

RESULT 40
LOCUS I44602 64 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 31 from patent US 5635352.
ACCESSION I44602
VERSION I44602.1 GI:2469315
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 64)
AUTHORS Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
TITLE Solution phase nucleic acid sandwich assays having reduced background noise
JOURNAL Patent: US 5635352-A 31 03-JUN-1997;
FEATURES
source 1..64
/organism="unknown"
BASE COUNT 18 a 16 c 17 g 13 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 64;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctgcgaagcaccctatcagcagt 24
|||||
Db 23 CTGCGAAGCACCCTATCAGCAGT 46

RESULT 41
LOCUS I71007 64 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 31 from patent US 5681697.
ACCESSION I71007
VERSION I71007.1 GI:3007142
KEYWORDS
SOURCE
ORGANISM
Unclassified.

Tue Aug 27 15:49:47 2002

us-10-037-990a-2.011.rge

Page 12

Search completed: August 26, 2002, 21:20:54
Job time: 7708 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 22:24:55 ; Search time 450.99 Seconds
(without alignments)
91.368 Million cell updates/sec

Title: US-10-037-990A-2

Perfect score: 24

Sequence: 1 ctgcgaagcaccctatcagcagt 24

Scoring table: OLIGO_NJC

Searched: 1736436 seqs, 858457221 residues

Word size: 21

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Minimum DB seq length: 0

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24: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	24	100.0	24	AA043144	HCV core region re
2	24	100.0	24	AA03586	HCV conserved regi
3	24	100.0	24	AA079963	Primer KY78 for HC
4	24	100.0	24	AA064900	Hepatitis C virus
5	24	100.0	24	AA093542	Antisense primer K
6	24	100.0	24	AA087095	HCV gene PCR prime
7	24	100.0	24	AAV18850	Primer KY78 for HC
8	24	100.0	24	AAV15319	Hepatitis C virus
9	24	100.0	24	AAZ09798	HCV PCR primer KY7

10	24	100.0	24	AA078452	HCV PCR primer 2.
11	24	100.0	24	AA023969	PCR primer KY78.
12	24	100.0	24	AA066753	PCR primer #2 used
13	24	100.0	24	AA025404	PCR primer used to
14	24	100.0	24	AA037587	HCV conserved regi
15	24	100.0	26	AA068061	Primer HCP96 for
16	24	100.0	26	AA064901	Hepatitis C virus
17	24	100.0	26	AA057408	Hepatitis C virus
18	24	100.0	27	AA071839	PCR primer for hep
19	24	100.0	27	AA074624	HCV-specific ampli
20	24	100.0	27	AA087367	Hepatitis C virus
21	24	100.0	27	ABA02736	Nucleic acid senso
22	24	100.0	27	ABA02738	Nucleic acid senso
23	24	100.0	27	AA078439	PCR primer used to
24	24	100.0	27	AA078441	PCR primer used to
25	24	100.0	27	ABK09262	Enzymatic nucleic
26	24	100.0	27	ABK09264	Enzymatic nucleic
27	24	100.0	28	AA05222	Hepatitis C virus
28	24	100.0	28	AA057757	Hepatitis C virus
29	24	100.0	30	AA055728	Hepatitis C detect
30	24	100.0	33	AA031158	Probe 127 for geno
31	24	100.0	33	AA046464	Hepatitis C virus
32	24	100.0	33	AAV07838	HCV.33.9 amplifier
33	24	100.0	33	AAV83066	Amplifier probe HC
34	24	100.0	40	AAV54436	Nucleotide sequenc
35	24	100.0	53	AA098139	Control label exte
36	24	100.0	53	AA098104	Label extender pro
37	24	100.0	57	AA063223	Hepatitis C virus
38	24	100.0	59	AA023543	HCV DNA fragment 2
39	24	100.0	59	AA0209795	HCV DNA probe. Sy
40	24	100.0	64	AA098121	Label extender pro
41	23	95.8	23	AA053257	Hepatitis C virus
42	23	95.8	29	AA037588	HCV conserved regi
43	23	95.8	29	AA064902	Hepatitis C virus
44	22	91.7	22	AA053259	Hepatitis C virus
45	22	91.7	22	AA025564	HCV RNA 5' UTR amp
46	22	91.7	23	AA025666	Oligonucleotide #1
47	22	91.7	24	AA019057	Hepatitis viral DN
48	22	91.7	52	AAA29435	Hepatitis C virus
49	21	87.5	25	AA079082	HCV PCR primer SEQ
50	21	87.5	27	AA067195	Hepatitis C virus
51	21	87.5	27	AA074623	HCV-specific ampli
52	21	87.5	28	AA070245	Hepatitis C virus
53	21	87.5	28	AA067194	Hepatitis C virus
54	21	87.5	28	AAV59059	Primer S778A for
55	21	87.5	28	AA057785	Hepatitis C virus
56	21	87.5	28	AA025414	Reverse PCR primer
57	21	87.5	46	AA058265	Hepatitis C virus

ALIGNMENTS

RESULT 1	AA043144/C
ID	AA043144 standard; DNA; 24 BP.
XX	
AC	AA043144;
XX	
DT	23-SEP-1993 (first entry)
XX	
DE	HCV core region reverse transcription primer #2.
XX	
KW	Non-coding region; hepatitis C virus; blood donor; type 2; type 1;
KW	HCV; NS-5; phylogeny; differentiation; NS-3; core region; type 3;
KW	PCR; amplify; polymerase chain reaction; primer; NS4; ss.
OS	Synthetic.
XX	
PN	WO9310239-A.
XX	
PD	27-MAY-1993.
XX	

```
PF 20-NOV-1992: 92WO-GB02143.
XX
XX 21-NOV-1991: 91GB-0024696.
PR 24-JUN-1992: 92GB-0013362.
XX
PA (COMM-) COMMON SERVICES AGENCY.
PI Chan S, Simmonds P, Yap PL.
XX
XX WPI: 1993-182554/22.
DR
XX
XX DNA encoding antigenic peptide(s) of new types of hepatitis C
PT virus - for diagnosing and treating HCV infection, screening
PT blood samples and identifying different HCV types
XX
XX Disclosure: Page 44; 120pp; English.
XX
XX The sequences given in AAQ3143-46 are primers which were used to
CC reverse transcribe the core region of the hepatitis C virus (HCV)
CC genome for sequence analysis. Analysis of regions of the HCV genome
CC revealed the existence of three distinct groups of HCV. Analysis of
CC the region encompassing -255 to -62 of the 5' non coding region (NCR)
CC (see AAQ43058-75) showed a difference of 9-14% in the nucleotide
CC sequences between the three groups. Two of the groups identified
CC were similar to those of HCV variants termed type 1 and 2, whilst the
CC third appeared to represent a novel type of virus. Comparison of the
CC NS3 region (see AAR37927-30) showed a high degree of sequence diversity
CC with type 3 being phylogenetically different to type 1 and 2. The
CC same degree differentiation was noted in the NS-5 (see AAR37923-26),
CC core region (see AAR37931) and the NS4 region (see AAQ3106-111) between
CC type 3 and type 1 sequences.
XX
SQ Sequence 24 BP; 4 A; 5 C; 9 G; 6 T; 0 other;

Query Match 100.0%; Score 24; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctcgcaagcaccctatcagcagc 24
Db 24 CTCGCAAGCACCCTATCAGCAGC 1

RESULT 2
AAQ37586
ID AAQ37586 standard; DNA; 24 BP.
XX
XX AAQ37586;
AC
XX
XX 23-JUN-1993 (first entry)
DT
XX
XX HCV conserved region downstream primer/probe KY78, position 276-299.
DE
XX
XX Polymerase chain reaction; PCR; amplify; primer; probe; hepatitis C;
KM virus; HCV; conserved region; RNA; open reading frame; polypeptide;
KM prototype; untranslated region; UTR; 5'UTR; conserved; replication;
KM regulation; US; Japan; C9; ss.
XX
XX Synthetic.
OS
XX
XX EP529493-A.
PN
XX
XX 03-MAR-1993.
PD
XX
XX 19-AUG-1992; 92EP-0114115.
PF
XX
XX 27-AUG-1991; 91US-0751305.
PR 21-JUL-1992; 92US-0918844.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA
XX Resnick RM, Young KKY;
PI
```

```
XX
XX WPI: 1993-068572/09.
DR
XX
XX Compasn. comprising oligo:nucleotide probe-primer - used for
PT detecting hepatitis C virus strains Japan, US and C9
PT
XX
XX Claim 3; Page 8; 43pp; English.
XX
XX The sequences given in AAQ37569-96 are oligonucleotides which can be
CC used as primers or probes which hybridise to the conserved region at
CC the 5'-end of the hepatitis C virus (HCV) genome. HCV is a small
CC RNA virus containing a small, positive sense, molecule of RNA about
CC 10,000 nucleotides in length. the genome contains a single, large,
CC open reading frame believed to translated in to a single, large,
CC polypeptide and subsequently processed. The open reading frame
CC begins at nucleotide 343 (using the numbering system from the
CC prototype virus) following an untranslated region (UTR) the 5'UTR
CC sequence is relatively conserved and may be important in viral
CC replication and regulation. The 5' end of the coding region is also
CC conserved. These primer/probes can be used to identify different HCV
CC isolates such as US, Japan and C9 (see also AAQ37597-601).
XX
SQ Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctcgcaagcaccctatcagcagc 24
Db 1 ctcgcaagcaccctatcagcagc 24

RESULT 3
AAQ79963
ID AAQ79963 standard; DNA; 24 BP.
XX
XX AAQ79963;
AC
XX
XX 01-AUG-1995 (first entry)
DT
XX
XX Primer KY78 for HCV RNA.
DE
XX
XX Primer: PCR; polymerase chain reaction; amplification;
KM RNA detection; reverse transcription; hepatitis C virus; HCV;
KM ss.
XX
XX Synthetic.
OS
XX
XX EP632134-A.
PN
XX
XX 04-JAN-1995.
PD
XX
XX 20-JUN-1994; 94EP-0109468.
PF
XX
XX 01-JUL-1993; 93US-0086483.
PR
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA
XX
XX Gelfand DH, Myers JW, Sliqua CL;
PI
XX
XX WPI: 1995-037815/06.
DR
XX
XX Improved amplification method for target RNA - using buffering
PT agent which buffers both pH and divalent cation concn.
PT
XX
XX Example 6; Page 22; 37pp; English.
XX
XX The primers given in AAQ79963-64 were used to amplify HCV templates
CC for use in a novel method of RNA amplification involving
CC high-temp. reverse transcription and PCR.
CC
```

SQ Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcagcgagt 24
|||||
Db 1 ctgcgaagcaccctatcagcgagt 24

RESULT 4

AAT64900
ID AAT64900 standard; DNA; 24 BP.

AC AAT64900;

DT 12-MAR-1998 (first entry)

DE Hepatitis C virus (HCV) oligonucleotide KY78.

KM Hepatitis C virus; reverse transcription; probe; PCR primer;

XX detection; ss.

OS Synthetic.

XX Hepatitis C virus.

PN EP787807-A2.

XX 06-AUG-1997.

PF 19-AUG-1992; 92EP-0065347.

PR 21-JUL-1992; 92US-0918844.

PR 27-AUG-1991; 91US-0751305.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

PI Resnick RM, Young KKY;

DR WPI: 1997-387489/36.

XX Oligo:nucleotide probes and primers for detecting hepatitis C virus

PT nucleic acid - from many different strains without loss of

PT specificity, allow single step reverse transcription and

PT amplification

XX Claims 4 and 5; Page 8; 35pp; English.

PS This oligonucleotide KY78 can be used as a probe for detecting

CC hepatitis C virus (HCV) nucleic acid from a Japanese or US prototype

CC strain as well as HCV C9 prototype strain. This oligonucleotide can

CC also be used as a primer for amplifying HCV nucleic acid. The sequence

CC of this oligonucleotide is contained in a specific region of HCV genomic

CC nucleic acid. The probe or the primer is preferably labelled. The probe

CC is used to detect HCV nucleic acid, preferably after this has been

CC amplified using the new primer in reverse transcription polymerase chain

CC reaction (RT-PCR), for both diagnostic and epidemiological applications.

CC The primer is effective for both reverse transcription and PCR,

CC eliminating the need to open the reaction tube during the procedure.

CC Amplification is effective (no need for a second round of PCR with nested

CC primers) and provides high sensitivity. The probe is directed to

CC conserved regions and so can detect many different strains without loss

CC of specificity.

XX Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;

SQ

OY 1 ctgcgaagcaccctatcagcgagt 24
|||||
Db 1 ctgcgaagcaccctatcagcgagt 24

RESULT 5

AAT93542
ID AAT93542 standard; DNA; 24 BP.

AC AAT93542;

DT 19-FEB-1998 (first entry)

DE Antisense primer KY78 for amplification of HCV RNA.

KM Armoured RNA; bacteriophage MS2; RT-PCR; ribonuclease; recombinant;

KM Human immunodeficiency virus; HIV; Hepatitis C virus; HCV; viral RNA;

KM detection; quantification standard; maturase protein; coat protein;

KM PCR primer; OS RNA; reverse transcriptase-PCR; ss.

XX Synthetic.

OS Hepatitis C virus.

PN US5677124-A.

PD 14-OCT-1997.

PF 03-JUL-1996; 96US-0675153.

PR 03-JUL-1996; 96US-0675153.

PA (AMBI-) AMBION INC.

PA (CENE-) CENETRON DIAGNOSTICS LLC.

PI Dubois DB, Pasloske BL, Winkler MM;

DR WPI: 1997-511866/47.

XX Recombinant RNA segment encapsidated in bacteriophage viral coat

PT protein - RNA detection and/or quantification standard

XX Example 5; Column 22; 23pp; English.

PS This antisense primer is used in the RT-PCR amplification of HCV RNA to

CC create a quantitative HCV "armoured RNA" standard. An "armoured RNA" is

CC a recombinant RNA segment encapsidated in bacteriophage viral coat

CC protein. The recombinant RNA segment comprises an operator coding

CC sequence, a viral maturase protein binding site, and a non-bacteriophage

CC sequence. The recombinant RNA in its packaged form is highly resistant to

CC ribonucleases, insuring that the RNA standard is not compromised by

CC inadvertent ribonuclease contamination. The armoured RNA standards are

CC ideal as RNA standards for the quantification of RNA viruses such as HIV

CC and HCV from human body fluids such as blood and cerebrospinal fluid.

XX Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;

SQ

Query Match 100.0%; Score 24; DB 18; Length 24;

Best Local Similarity 100.0%; Pred. No. 4.4e-05;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcagcgagt 24
|||||
Db 1 ctgcgaagcaccctatcagcgagt 24

RESULT 6

AAT87095
ID AAT87095 standard; DNA; 24 BP.

AC AAT87095;

DT 07-JAN-1998 (first entry)

```
XX DE HCV gene PCR primer KY78.
XX PR RNA; plasma; hepatitis C virus; HCV; primer; PCR;
XX KW polymerase chain reaction; ss.
XX OS Synthetic.
XX PN US5654179-A.
XX PD 05-AUG-1997.
XX PF 14-NOV-1990; 900S-0614921.
XX PR 08-APR-1993; 930S-0044649.
XX PR 14-NOV-1990; 900S-0614921.
XX PR 19-JUN-1992; 920S-0901545.
XX PR 03-OCT-1994; 940S-0317220.
XX PA (HYDS ) HRI RES INC.
XX PI Lin L;
XX DR WPI: 1997-401849/37.
XX PT Preparation of RNA samples from plasma - by alcohol precipitation
XX PT after lysis with guanidinium thiocyanate
XX PS Disclosure: Column 47; 60pp; English.
XX CC Primer KY78 (AA187095) and primer KY80 (AA187096) were used for the
XX CC PCR amplification of a 305 bp hepatitis C virus gene product (see
XX CC AA187088). A claimed method for preparing RNA samples comprises: (a)
XX CC mixing plasma with an aqueous buffer solution containing guanidinium
XX CC thiocyanate and beta-mercaptoethanol; (b) heating the mixture; (c)
XX CC adding an equal volume of an alcohol to precipitate RNA; and (d)
XX CC recovering the RNA. The method can be used to prepare RNA samples
XX CC for subsequent amplification, especially for detecting pathogens,
XX CC e.g. hepatitis C virus or HIV. Compared with the known "IsoQuick"
XX CC and "RNAzol" methods, the method uses fewer tubes (just one),
XX CC requires fewer steps, takes less time and produces no toxic waste.
XX SO Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 18; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctcgcagcaccctatcagcagc 24
   |||||||||||||||||||||
DB 1 ctcgcagcaccctatcagcagc 24

RESULT 7
AAV18850
ID AAV18850 standard; DNA; 24 BP.
XX AC AAV18850;
XX DT 11-JUN-1998 (first entry)
XX DE Primer KY78 for HCV DNA.
XX KW PCR primer; HCV; nucleic acid standard; Armored RNA; ss.
XX OS Synthetic.
XX OS Hepatitis virus.
XX PN WO9800547-A1.
XX PD 08-JAN-1998.
XX
```

```
PF 02-JUL-1997; 97WO-US12551.
XX 24-JUN-1997; 97US-0881571.
XX 03-JUL-1996; 96US-0021145.
XX 03-JUL-1996; 96US-0675153.
XX (AMBI-) AMBION INC.
XX PA (CENE-) CENETRON DIAGNOSTICS LLC.
XX PI Dubois DB, Pasloske BL, Winkler MM;
XX DR WPI: 1998-086972/08.
XX PR Ribonuclease resistant RNA molecules and their production - useful
XX PT as standards in quantitative PCR for pathogens, e.g HIV-1, HIV-2 and
XX PT HCV
XX PS Example 5; Page 41; 134pp; English.
XX CC The present sequence is a primer for hepatitis C virus (HCV) DNA,
XX CC which was used in the preparation of a nucleic acid standard,
XX CC comprising a nuclease resistant nucleic acid segment encoding a
XX CC standard nucleic acid, i.e. RNA. The ribonuclease resistant RNA
XX CC standard, designated Armored RNA (RM) is useful as an internal or
XX CC external nucleic acid standard in quantitative assays, e.g. PCR or
XX CC RT-PCR for the presence of a tested nucleic acid in blood samples.
XX SO Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;
```

```
Query Match 100.0%; Score 24; DB 19; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctcgcagcaccctatcagcagc 24
   |||||||||||||||||||||
DB 1 ctcgcagcaccctatcagcagc 24
```

```
RESULT 8
AAV15319
ID AAV15319 standard; DNA; 24 BP.
XX AC AAV15319;
XX DT 28-MAY-1998 (first entry)
XX DE Hepatitis C virus PCR primer PKY78.
XX KW Hepatitis C virus; HCV; PCR primer; detection; reverse transcription;
XX KW enzyme immunoassay; viral RNA; ss.
XX OS Synthetic.
XX OS Hepatitis C virus.
XX PN WO9746716-A1.
XX PD 11-DEC-1997.
XX PR 03-JUN-1997; 97WO-IT00128.
XX PR 07-JUN-1996; 96IT-M000404.
XX PA (WESA ) WABCO BV.
XX PI Bosio P, Clemenza F, Strumia C;
XX DR WPI: 1998-042222/04.
XX PT Detection of hepatitis C virus - by reverse transcription,
XX PT single-step PCR and detection by DNA enzyme immunoassay
XX PS Disclosure; Page 4; 26pp; English.
```

XX The present sequence represents a PCR primer involved in the method of
CC the present invention for detecting hepatitis C virus (HCV). The method
CC comprises: (a) reverse-transcribing the viral RNA; (b) amplifying the
CC resulting cDNA by a single polymerase chain reaction in a reaction
CC mixture having a Mg²⁺/Taq polymerase ratio of about 100 nmole/enzyme
CC unit; and (c) detecting the amplification product by DEIA (DNA enzyme
CC immunassay) using an oligonucleotide probe. The sensitivity of this
CC method is at least equal to that achievable by more complicated assays
CC using nested PCR.
XX
SQ Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;
Query Match 100.0%; Score 24; DB 19; Length 24;
Best Local Similarity 100.0%; Pred. No. 4,4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ctgcgaagaccctatcagcagt 24
Db 1 ctgcgaagaccctatcagcagt 24
RESULT 9
AAZ09798
ID AAZ09798 standard; DNA: 24 BP.
XX
AC AAZ09798;
XX
DT 26-NOV-1999 (first entry)
XX
DE HCV PCR primer KY78.
XX
KW Probe; amplification; primer; reporter group; quencher group; PCR;
KM amplicon; detection; ss.
XX
OS Synthetic.
OS Hepatitis C virus.
OS
PN DE19814001-A1.
PN
PD 30-SEP-1999.
PD
PF 28-MAR-1998; 98DE-1014001.
PF
PR 28-MAR-1998; 98DE-1014001.
PR
XX (HOFF) ROCHE DIAGNOSTICS GMBH.
PA
XX Kessler C, Habershausen G, Batz H, Orum H;
PI
XX WPI; 1999-552213/47.
DR
XX Fluorescent nucleic acid amplification assay, useful for detection of
PT viral, bacterial, cellular, yeast or fungal nucleic acids
PT
XX Example 1; Page 19; 16pp; German.
PS
XX This invention describes a novel assay for a nucleic acid which comprises
CC an amplification reaction using two non-overlapping primers, a polymerase
CC with 5'-nuclease activity and a probe with reporter groups and quencher
CC groups that binds a region other than that bound by the primers. The
CC reaction generates products of less than 100 nucleotides. The assay is
CC useful for detection of viral, bacterial, cellular, yeast or fungal
CC nucleic acids in human, animal, bacterial, plant, yeast or fungal
CC samples, e.g. feces, smears, cell suspensions, cultures or tissue, cell
CC or liquid biopsy samples. Compared with assays in which longer
CC amplification products are generated, the assay can be performed more
CC rapidly using shorter polymerase chain reaction (PCR) cycles, sensitivity
CC may be increased due to reduced competition between the short
CC counterstand of the amplicon and the detector probe. Specificity may
CC also be increased because of the increased relative length of sequence B
CC compared with the total length of the amplicon and the differentiability

CC of subtypes may be increased. In addition signal-to-noise ratios may be
CC increased with the new method because short amplicons have reduced
CC potential for nonspecific hybridization. In addition reproducibility may
CC be increased because small target regions on RNA genomes are less
CC sensitive to RNA degradation, and the possibilities for secondary
CC structure formation are reduced. This sequence represents a PCR primer
CC used in the amplification of a region of HCV which is used to illustrate
CC the method of the invention.
XX
SQ Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;
Query Match 100.0%; Score 24; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 4,4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ctgcgaagaccctatcagcagt 24
Db 1 ctgcgaagaccctatcagcagt 24
RESULT 10
AAZ78452
ID AAZ78452 standard; DNA: 24 BP.
XX
AC AAZ78452;
XX
DT 26-AUG-1999 (first entry)
XX
DE HCV PCR primer 2.
XX
KW RNA standard; HCV; detection; gag gene; cerebrospinal fluid; PCR primer;
KM ribonuclease resistant; encapsulation; viral; HIV-1; HIV-2; HCV;
XX HTLV-1; HTLV-2; hepatitis G; enterovirus; blood-borne pathogen; ss.
XX
OS Synthetic.
OS Hepatitis C virus.
OS
PN US5919625-A.
PN
PD 06-JUL-1999.
PD
PF 29-APR-1997; 97US-0841252.
PF
PR 03-JUL-1996; 96US-0675153.
PR
PR 29-APR-1997; 97US-0841252.
PR
XX (AMBI-) AMBION INC.
PA (CENE-) CENETRON DIAGNOSTICS LLC.
PA
XX Dubois DB, Pasloske BL, Winkler MM;
PI
XX WPI; 1999-394617/33.
DR
XX Ribonuclease resistant viral RNA standards
PT
XX Example V; Column 31-32; 22pp; English.
PS
XX This invention describes the construction of novel RNA standards for the
CC quantification of human immunodeficiency virus (HIV) and hepatitis C
CC virus (HCV) from e.g. cerebrospinal fluids. The method involves (1)
CC obtaining a sample to be analysed; (2) obtaining a ribonuclease resistant
CC RNA standard, encapsulated in a bacteriophage viral coat protein, which
CC comprises an RNA segment having a segment encoding a sequence that serves
CC as a standard in detection or quantification of the RNA of interest;
CC (3) mixing the sample with the standard; (4) isolating RNA from the
CC mixture; and (5) assaying for the presence of the RNA. The method is
CC useful for the detection or quantification of HIV-1, HIV-2, HCV, HTLV-1,
CC HTLV-2, hepatitis G, an enterovirus, or a blood-borne pathogen. This
CC sequence represents a PCR primer used to amplify a region of the
CC Hepatitis C genome which is used in the method of the invention.
XX
SQ Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 20; Length 24;
 Best Local Similarity 100.0%; Pred. No. 4.4e-05;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctcgaagcaccctatcagcagt 24
 |||||||
 Db 1 ctcgaagcaccctatcagcagt 24

RESULT 11

AAH23969
 ID AAX23969 standard; DNA; 24 BP.

XX AAX23969;

DT 28-JUN-1999 (first entry)

DE PCR primer KY78.

XX Amplification: medical; forensic; diagnosis; food analysis; blood;
 KW environmental analysis; plant protection; veterinary medicine;
 KW human immune deficiency virus; hepatitis B; hepatitis C; Chlamydia;
 KW screening; PCR primer; detection; probe; ss.

OS Synthetic.

PN DE19748690-A1.

PD 06-MAY-1999.

PF 04-NOV-1997; 97DE-1048690.

PR 04-NOV-1997; 97DE-1048690.

PA (HOFF) ROCHE DIAGNOSTICS GMBH.

DR WPI; 1999-278780/24.

XX Detecting nucleic acid by generating short amplicons and probing
 PT e.g. for diagnosis, food and environmental analysis and plant
 PT protection

PS Example 1; Page 17; 22pp; German.

XX This invention describes a method for the detection of nucleic acid
 CC which comprises amplification and reaction of the amplicon with a probe.
 CC The method is used to detect nucleic acid e.g. for medical or forensic
 CC diagnosis, in food and environmental analysis, in plant protection and
 CC veterinary medicine, e.g. for detecting human immune deficiency virus,
 CC hepatitis B or C viruses, or Chlamydia, in blood screening. The method
 CC provides target-dependent, exponential amplification for highly specific
 CC and sensitive, reproducible and quantitative detection of one or more
 CC nucleic acids (single or double stranded). The design of primers and
 CC probes is sufficiently flexible to allow many nucleic acids to be
 CC detected in a standardized reaction format using partly the same primers
 CC and probes. Only small amplicons are produced (requiring short
 CC amplification cycles), there is no competition/displacement between the
 CC short counter-strand of the amplicon and the detection probe, and
 CC specificity is high because the relative proportion of the internal
 CC detection region is increased with respect to the total amplicon length,
 CC allowing better differentiation between (viral) subtypes. Also short
 CC amplicons are less likely to undergo non-specific hybridization, so
 CC background is low, and short RNA sequences are more stable, with reduced
 CC tendency to form secondary structures. AAX23968-69 and AAX24035-37 are
 CC PCR primers and probes used in the method of the invention.

SQ Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 20; Length 24;
 Best Local Similarity 100.0%; Pred. No. 4.4e-05;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 ctcgaagcaccctatcagcagt 24
 |||||||
 Db 1 ctcgaagcaccctatcagcagt 24

RESULT 12

AAC6753/C
 ID AAC6753 standard; DNA; 24 BP.

XX AAC6753;

DT 16-FEB-2001 (first entry)

DE PCR primer #2 used for detecting Hepatitis C virus.

XX PCR primer; virus detection; HCV core protein; ss.

OS Hepatitis C virus.

PN WO200063444-A2.

PD 26-OCT-2000.

PF 14-APR-2000; 2000WO-EP04175.

PR 14-APR-1999; 99US-0129319.

PA (INSP) INST PASTEUR.

PI Budkowska A, Maillard P, Nickiewicz J, Crainic R;

DR WPI; 2000-679609/66.

XX Directly detecting hepatitis C virus in serum of patients comprises use
 PT of primers corresponding to viral RNA encoding core protein, or
 PT monoclonal antibodies recognizing core protein or nucleocapsid protein
 PT of the virus -

PS Claim 1; Page 22; 22pp; English.

XX The present invention relates to a method for directly detecting
 CC hepatitis C virus (HCV) in fractionated or non-fractionated serum of a
 CC patient. The method comprises detecting virus with primers corresponding
 CC to viral RNA encoding core protein. The present sequence is one such
 CC primer of the present invention. The method allows visualisation of the
 CC presence of the HCV by a double sandwich test. HCV core protein has a
 CC number of important roles, including modulation of transcription from
 CC cellular promoters, suppression of the HBV gene expression, interaction
 CC with the cytoplasmic tail of lymphotoxin receptor, as well as an
 CC important role in viral replication.

SQ Sequence 24 BP; 4 A; 5 C; 9 G; 6 T; 0 other;

Query Match 100.0%; Score 24; DB 21; Length 24;
 Best Local Similarity 100.0%; Pred. No. 4.4e-05;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctcgaagcaccctatcagcagt 24
 |||||||
 Db 24 CTCGACAGCACCTATCAAGCAGT 1

RESULT 13

AAH25404
 ID AAH25404 standard; DNA; 24 BP.

XX AAH25404;

DT 22-AUG-2001 (first entry)

```

XX PCR primer used to amplify a HCV DNA fragment.
XX
KW Magnetic glass particle; nucleic acid purification; PCR primer; ss.
XX
OS Hepatitis C virus.
XX
PN WO200137291-A1.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-EP11459.
XX
XX 17-NOV-1999; 99EP-0122853.
PR 12-MAY-2000; 2000EP-0110165.
XX
PA (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI Weindel K, Riedling M, Geiger A;
XX
DR WPI; 2001-381247/40.
XX
PT Novel composition of magnetic glass particles for purification of DNA
PR or RNA in automated processes
XX
PS Example 7; Page 95; 105pp; English.
XX
CC The specification describes a composition of magnetic glass particles,
CC which contain at least one magnetic object with a mean diameter between
CC 5-500 nm. The composition is useful for the purification of nucleic
CC acids. The composition can be used to process large quantities of
CC nucleic acid samples, because it does not involve the particles being
CC centrifuged or the fluids being drawn through glass fiber filters.
CC PCR primers AAH25403-04 were used to amplify HCV DNA fragments. The
CC amplified fragment can be purified using the method of the invention.
XX
SO Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 22; Length 24;
Best Local Similarity 100.0%; Pred. No. 4,4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcagcgact 24
   |||||||
DB 1 ctgcgaagcaccctatcagcgact 24

RESULT 14
AAO37587
ID AAO37587 standard; DNA; 26 BP.
XX
AC AAO37587;
XX
DT 23-JUN-1993 (first entry)
XX
DE HCV conserved region downstream primer/probe KY145, position 276-301.
XX
KW Polyomerase chain reaction; PCR; amplify; primer; probe; hepatitis C;
KW virus; HCV; conserved region; RNA; open reading frame; polyprotein;
KW prototype; untranslated region; UTR; 5'UTR; conserved; replication;
XX regulation; US; Japan; C9; ss.
XX
OS Synthetic.
XX
FN EP529493-A.
XX
PD 03-MAR-1993.
XX
PF 19-AUG-1992; 92EP-0114115.
XX
XX 27-AUG-1991; 91US-0751305.
PR 21-JUL-1992; 92US-0918844.
XX

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PA	(HOFF) HOFFMANN LA ROCHE & CO AG F.
XX	
PI	Resnick RM, Young KKY;
XX	
DR	WPI; 1993-068572/09.
XX	
PT	Compsn. comprising oligo:nucleotide probe-primer - used for
PT	detecting hepatitis C virus strains Japan, US and C9
XX	
PS	Claim 3; Page 8; 43pp; English.
XX	
CC	The sequences given in AAQ37569-96 are oligonucleotides which can be
CC	used as primers or probes which hybridise to the conserved region at
CC	the 5'-end of the hepatitis C virus (HCV) genome. HCV is a small
CC	RNA virus containing a small, positive sense, molecule of RNA about
CC	10,000 nucleotides in length. the genome contains a single, long,
CC	open reading frame believed to translated in to a single, large
CC	polyprotein and subsequently processed. The open reading frame
CC	begins at nucleotide 343 (using the numbering system from the
CC	prototype virus) following an untranslated region (UTR) the 5'UTR
CC	sequence is relatively conserved and may be important in viral
CC	replication and regulation. The 5' end of the coding region is also
CC	conserved. These primer/probes can be used to identify different HCV
CC	isolates such as US, Japan and C9 (see also AAQ37597-601).
XX	
SO	Sequence 26 BP; 7 A; 10 C; 5 G; 4 T; 0 other;
	Query Match 100.0%; Score 24; DB 14; Length 26;
	Best Local Similarity 100.0%; Pred. No. 4,4e-05;
	Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 ctgcgaagcaccctatcagcagcagt 24
DB	3 ctgcgaagcaccctatcagcagcagt 26
	RESULT 15
AAQ68061	
ID	AAQ68061 standard; DNA; 26 BP.
XX	
AC	AAQ68061;
XX	
DT	19-DEC-1994 (first entry)
XX	
DE	Primer HcPr96 for HCV genotyping (universal).
XX	
KW	Hepatitis C virus; HCV; probe; genotyping; hybridisation;
KW	non-A, non-B hepatitis; NANBH; amplification; primer;
KW	polymerase chain reaction; PCR; ss.
XX	
OS	Synthetic.
XX	
PN	WO9412670-A.
XX	
PD	09-JUN-1994.
XX	
PF	26-NOV-1993; 93WO-EP03325.
XX	
XX	27-NOV-1992; 92EP-0403222.
PR	31-AUG-1993; 93EP-0402129.
XX	
PA	(INNO-) INNOGENETICS NV SA.
PI	
PI	Maertens G, Rossau R, Stuyver L, Van Heuverswyn H;
XX	
DR	WPI, 1994-200296/24.
XX	
PT	Process for genotyping Hepatitis C virus (HCV) isolates -
PT	utilises probes hybridising to HCV isolate domains
XX	
PS	Claim 13; Page 73; 96pp; English.
XX	

CC Genotyping HCV utilises probes hybridising to HCV isolate domains.
CC HCV types 2, 3, 4, 5 or 6 and subtypes 1a, 1b, 2a, 2b, 3a, 3b,
CC 3c, 4c, 4d, 4e, 4f, 4g and 4h can be typed.
CC The hybridisation step is pref. preceded by an amplification
CC step (PCR) using universal primers given in AA068058-61.

XX
SQ Sequence 26 BP; 7 A; 10 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 15; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcagcagt 24
|||||
DB 3 ctgcgaagcaccctatcagcagt 26

RESULT 16
AA064901

ID AA064901 standard; DNA; 26 BP.

XX
AC AA064901;

XX 12-MAR-1998 (first entry)

DE Hepatitis C virus (HCV) oligonucleotide KY145.

XX
KM Hepatitis C virus; reverse transcription; probe; PCR primer;
KM detection; ss.

OS Synthetic.

XX Hepatitis C virus.

PN EP787807-A2.

XX 06-AUG-1997.

PF 19-AUG-1992; 92EP-0065347.

PR 21-JUL-1992; 92US-0918844.

PR 27-AUG-1991; 91US-0751305.

PA (HOPE) HOFFMANN LA ROCHE & CO AG F.

PI Resnick RM, Young KKY;

DR WPI: 1997-387489/36.

XX
PT Oligo:nucleotide probes and primers for detecting hepatitis C virus
PT specificity, allow single step reverse transcription and
PT amplification

PS Claims 4 and 5; Page 8; 35pp; English.

CC This oligonucleotide KY145 can be used as a probe for detecting
CC hepatitis C virus (HCV) nucleic acid from a Japanese or US prototype
CC strain as well as HCV C9 prototype strain. This oligonucleotide can
CC also be used as a primer for amplifying HCV nucleic acid. The sequence
CC of this oligonucleotide is contained in a specific region of HCV genome
CC nucleic acid. The probe or the primer is preferably after this has been
CC is used to detect HCV nucleic acid, preferably after this has been
CC amplified using the new primer in reverse transcription polymerase chain
CC reaction (RT-PCR), for both diagnostic and epidemiological applications.
CC The primer is effective for both reverse transcription and PCR,
CC eliminating the need to open the reaction tube during the procedure.
CC Amplification is effective (no need for a second round of PCR with nested
CC primers) and provides high sensitivity. The probe is directed to
CC conserved regions and so can detect many different strains without loss
CC of specificity.

XX
SQ Sequence 26 BP; 7 A; 10 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 18; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcagcagt 24
|||||
DB 3 ctgcgaagcaccctatcagcagt 26

RESULT 17
AA057408

ID AA057408 standard; DNA; 26 BP.

XX
AC AA057408;

XX 07-APR-2000 (first entry)

DE Hepatitis C virus PCR primer A5'-II SEQ ID NO:23.

XX
KM Hepatitis C virus; RNA virus; replication; viral infection;
KM PCR primer; ss.

XX Hepatitis C virus.

PN WO967394-A1.

XX 29-DEC-1999.

PF 24-JUN-1999; 99WO-IP03380.

PR 24-JUN-1998; 98JP-0177820.

PA (CHUS) CHUGAI SEIYAKU KK.

XX Kohara M, Kohara K, Taira K, Matsuzaki J, Ohmori H;

DR WPI: 2000-106296/09.

XX
PT Vectors expressing full-length gene of RNA viruses, useful in
PT clarifying mechanisms of RNA viral replication, infection, and
PT developing remedies and therapeutics

PS Example 2; Page 21; 46pp; Japanese.

CC The present invention describes a vector comprising a cDNA encoding an
CC RNA virus gene, constructed to ensure the exact and homogeneous
CC transcription of both terminals of the RNA virus gene. Also described
CC is a method for screening drugs for inhibiting the replication of RNA
CC virus by using the RNA viral infection model animal, particularly one
CC with hepatitis C viral infection. The vector is useful in clarifying
CC the mechanism of RNA viral replication, onset of RNA viral infection,
CC and developing remedies and therapeutics for RNA viral infections,
CC particularly of a hepatitis C virus. The present sequence represents
CC a PCR primer which is used in the exemplification of the present
CC invention.

XX
SQ Sequence 26 BP; 7 A; 10 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 21; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcagcagt 24
|||||
DB 3 ctgcgaagcaccctatcagcagt 26

RESULT 18
AA071839

ID AA071839 standard; DNA; 27 BP.

```

XX AC AA071839;
XX XX
XX DT 25-MAR-1995 (first entry)
XX XX
DE PCR primer for hepatitis G virus.
XX KM DNA primer; sense; polymerase chain reaction; hepatitis G virus;
XX KM diagnostic; ss.
XX OS Synthetic.
XX PN W09418217-A.
XX PD 18-AUG-1994.
XX PF 03-FEB-1993; 93WO-US00928.
XX PR 03-FEB-1993; 93AU-0036061.
XX PR 03-FEB-1993; 93WO-US00928.
XX PA (ABBO ) ABBOTT LAB.
XX PI Heltzakis AE, Kuhn MC, Tassopoulos NC, Troonen H;
XX DR WPI; 1994-279671/34.
XX PT Hepatitis G virus polypeptides, nucleic acids, antibodies and cell
XX PT cultures - used to detect the virus in a test sample and to
XX PT screen antiviral agents
XX PS Disclosure; Page 60; 67pp; English.
XX CC The sense primer is used with an antisense primer (AA071840)
XX CC in a reverse transcription-polymerase chain reaction assay for
XX CC hepatitis E virus. A DNA probe (AA071841) is used to detect the PCR
XX CC products generated by the 2 primers.
XX SQ Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctgcgaagcaccctatcagcagc 24
   ||||||||||||||||||||
Db 3 ctgcgaagcaccctatcagcagc 26

RESULT 19
AAA74624
ID AAA74624 standard; DNA: 27 BP.
XX AC AAA74624;
XX AC
XX DT 08-JAN-2001 (first entry)
XX DT
XX DE HCV-specific amplification primer C287R27.
XX KM Hepatitis C virus; HCV; HCV detection; amplification primer; ss.
XX OS Hepatitis C virus.
XX PN EP1026262-A2.
XX PD 09-AUG-2000.
XX PF 01-FEB-2000; 2000EP-0300763.
XX PR 03-FEB-1999; 99US-0118497.
XX PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.

```

```

XX PI Linnen JM, Gorman KM;
XX DR WPI; 2000-507254/46.
XX XX
XX PT Detecting hepatitis C virus in biological sample involves amplifying
XX PT reverse transcribed products of virus RNA using amplification primers
XX PT whose sequences correspond to 5' or 3' non-coding region of the virus
XX PT RNA
XX PS Claim 30; Page 27; 28pp; English.
XX XX
XX CC The present sequence is an amplification primer used in a method for
XX CC detecting hepatitis C virus (HCV) RNA in biological samples. The HCV
XX CC RNA is reverse transcribed to generate cDNA. This is then amplified
XX CC using primers, including the present sequence, corresponding to the
XX CC 5' or 3' non-coding region of HCV. The method is useful for the
XX CC diagnosis of HCV infection in patients, in testing the efficacy of
XX CC anti-HCV therapeutic regimens, and in screening blood for HCV-infected
XX CC samples. The method provides an improved single-round, reverse
XX CC transcription/amplification assay which detects low copy levels of HCV
XX CC RNA. The primers and assay system are designed to allow the
XX CC co-amplification of multiple regions of the HCV genome, multiple viral
XX CC species, and an internal positive control (IPC) RNA (or DNA).
XX CC Simultaneous amplification/detection of multiple regions of the HCV
XX CC genome increases assay sensitivity and the co-amplification of an IPC
XX CC decreases the likelihood of false negative results because of PCR
XX CC inhibition.
XX SQ Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 other;

```

```

Query Match 100.0%; Score 24; DB 21; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctgcgaagcaccctatcagcagc 24
   ||||||||||||||||||||
Db 3 ctgcgaagcaccctatcagcagc 26

```

```

RESULT 20
AA287367
ID AA287367 standard; cDNA: 27 BP.
XX AC AA287367;
XX AC
XX DT 22-MAY-2000 (first entry)
XX DT
XX DE Hepatitis C virus 5'NCR RT-PCR primer NC4.
XX KM Hepatitis C virus; HCV; in vitro culture; primary mammalian hepatocyte;
XX KM culture medium; replication; drug screening; antibody testing;
XX KM diagnosis; vaccine development; 5'NCR; reverse transcriptase-PCR;
XX KM RT-PCR primer; ss.
XX OS Hepatitis C virus.
XX PN W09967362-A1.
XX PD 29-DEC-1999.
XX PF 23-JUN-1999; 99WO-EP04337.
XX PR 24-JUN-1998; 98EP-0401554.
XX PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX PI Rumlun S, Inchauspe G, Trepo C, Gripon P;
XX DR WPI; 2000-160580/14.
XX PT Use of a culture medium comprising at least one mammalian plasma or

```

```

PT enzymatic nucleic acid and one or more sensors -
XX
XX Example 1; Page 69; 115pp; English.
XX
XX The invention relates to a nucleic acid sensor molecule (I) comprising an
CC enzymatic nucleic acid component and one or more sensor components. (I)
CC is useful in diagnostic applications to identify the presence of genes
CC and/or gene products indicative of a particular genotype and/or
CC phenotype, e.g., a disease state or infection and for diagnosis of disease
CC states or physiological abnormalities related to the expression of viral,
CC bacterial or cellular RNA and DNA. (I) is useful in nucleic acid-based
CC electronics, for the detection of specific target signalling molecules,
CC in assays to assess the specificity, toxicity and effectiveness of
CC various small molecules, nucleoside analogues or non-nucleic acid drugs
CC or for detection of pathogens, biochemicals, organic or inorganic
CC compounds. The present sequence is that of a nucleic acid sensor molecule
CC of the invention.
XX
XX Sequence 27 BP; 8 A; 10 C; 5 G; 4 U; 0 other;
SQ
Query Match 100.0%; Score 24; DB 22; Length 27;
Best Local Similarity 83.3%; Pred. No. 4.4e-05;
Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0.
OY 1 ctgcgaagcaccctatcacgacagt 24
   |:|||||:|||||:|||||||:
Db 3 cucgcgaagcaccctcaucagcgagu 26
RESULT 22
ABA02738/C
ID ABA02738 standard; RNA; 27 BP.
XX
XX ABA02738;
AC
XX 12-FEB-2002 (first entry)
DT
XX Nucleic acid sensor molecule SEQ ID NO 10.
DE
XX Nucleic acid sensor molecule; detection; infection; disease diagnosis;
KW physiological abnormality; electronic; signalling molecule;
KW nucleoside analogue, ss.
KM
XX Synthetic.
OS
XX WO20016721-A2.
PN
XX 13-SEP-2001.
PD
XX 06-MAR-2001; 2001WO-US07163.
PE
XX 06-MAR-2000; 2000US-187128P.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Usman N, McSwiggen JA, Zinnen S, Seiwert S, Haerberl P;
PI Chowrira B, Blatt L;
PL
XX WPI; 2001-616242/71.
DR
XX New nucleic acid sensor molecule useful in diagnostic applications,
PT nucleic acid-based electronics and functional genomics, comprises an
PT enzymatic nucleic acid and one or more sensors -
XX
XX Example 1; Page 69; 115pp; English.

```

CC bacterial or cellular RNA and DNA. (1) is useful in nucleic acid-based
CC electronics, for the detection of specific target signalling molecules,
CC in assays to assess the specificity, toxicity and effectiveness of
CC various small molecules, nucleoside analogues or non-nucleic acid drugs
CC or for detection of pathogens, biochemicals, organic or inorganic
CC compounds. The present sequence is that of a nucleic acid sensor molecule
CC of the invention.

XX
SQ Sequence 27 BP; 4 A; 5 C; 10 G; 8 U; 0 other;

Query Match 100.0%; Score 24; DB 22; Length 27;
Best Local Similarity 100.0%; Pred. No. 4,4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcagcagc 24
DB 25 ctgcgaagcaccctatcagcagc 2

RESULT 23

ID AAH78439 standard; DNA; 27 BP.

AC AAH78439;

DT 10-DEC-2001 (first entry)

DE PCR primer used to amplify HCV cDNA fragment.

XX Protein isolation; magnetic colloidal particle; polymer envelope;

KW vaccine; HCV; PCR primer; ss.

XX Hepatitis C virus.

XX WO200152612-A2.

PD 26-JUL-2001.

PF 22-JAN-2001; 2001WO-FR00205.

PR 21-JAN-2000; 2000FR-0000862.

XX (INMR) BIO MERIEUX.

PI Elaissari A, Mandrand B, Delair T, Spencer D, Arkis A;

DR WPI: 2001-596423/67.

XX
PT Isolation of protein and protein-nucleic acid complexes, useful e.g.
PT for subsequent analysis or transport, by binding to magnetic beads
PT coated with functionalized polymer

XX Example 4; Page 13; 29pp; French.

XX The specification describes a method for the isolation of proteins
CC and/or their complexes with nucleic acid. The method comprises treating
CC a sample with magnetic colloidal particles that comprise a magnetic
CC core and an envelope of a polymer (P1) containing ionizable functional
CC groups. The mixture is incubated then the proteins or complexes are
CC recovered by application of a magnetic field. The core is covered by
CC at least one polymer (P2) containing functional groups, at least some
CC of which have reacted with groups in (P1). Functional groups in P1
CC and P2 are the same or different, and are amino, hydroxy thiol, formyl,
CC ester, anhydride, acyl chloride, carbonate, carbamate and/or
CC isothio)cyanate. The method is used for extraction, identification,
CC detection and/or quantification of protein and their complexes. It is
CC also used for establishing cell cultures and biological samples. The
CC complexes formed between magnetic colloidal particles and the proteins
CC are useful for transfer, transport and/or storage of infectious agents
CC (virus, bacterium or yeast) and for preparation of vaccines. PCR
CC primers AAH78438-39 were used to amplify a fragment of HCV cDNA. The
CC amplified fragment was used to demonstrate the use of the method of the

CC invention for capture of HCV particles by magnetic latex.

XX
SQ Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 22; Length 27;
Best Local Similarity 100.0%; Pred. No. 4,4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcagcagc 24
DB 2 ctgcgaagcaccctatcagcagc 25

RESULT 24

ID AAH78441 standard; DNA; 27 BP.

AC AAH78441;

DT 10-DEC-2001 (first entry)

DE PCR primer used to amplify HCV cDNA fragment.

XX Protein isolation; magnetic colloidal particle; polymer envelope;

KW vaccine; HCV; PCR primer; ss.

XX Hepatitis C virus.

XX WO200152612-A2.

PD 26-JUL-2001.

PF 22-JAN-2001; 2001WO-FR00205.

PR 21-JAN-2000; 2000FR-0000862.

XX (INMR) BIO MERIEUX.

PI Elaissari A, Mandrand B, Delair T, Spencer D, Arkis A;

DR WPI: 2001-596423/67.

XX
PT Isolation of protein and protein-nucleic acid complexes, useful e.g.
PT for subsequent analysis or transport, by binding to magnetic beads
PT coated with functionalized polymer

XX Example 4; Page 13; 29pp; French.

XX The specification describes a method for the isolation of proteins
CC and/or their complexes with nucleic acid. The method comprises treating
CC a sample with magnetic colloidal particles that comprise a magnetic
CC core and an envelope of a polymer (P1) containing ionizable functional
CC groups. The mixture is incubated then the proteins or complexes are
CC recovered by application of a magnetic field. The core is covered by
CC at least one polymer (P2) containing functional groups, at least some
CC of which have reacted with groups in (P1). Functional groups in P1
CC and P2 are the same or different, and are amino, hydroxy thiol, formyl,
CC ester, anhydride, acyl chloride, carbonate, carbamate and/or
CC isothio)cyanate. The method is used for extraction, identification,
CC detection and/or quantification of protein and their complexes. It is
CC also used for establishing cell cultures and biological samples. The
CC complexes formed between magnetic colloidal particles and the proteins
CC are useful for transfer, transport and/or storage of infectious agents
CC (virus, bacterium or yeast) and for preparation of vaccines. PCR
CC primers AAH78440-41 were used to amplify a fragment of HCV cDNA. The
CC amplified fragment was used to demonstrate the use of the method of the
CC invention for capture of HCV particles by magnetic latex.

XX
SQ Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 22; Length 27;

PA (CHOW/) CHOWRIRA B M.
XX
XX Blatt L, McSwiggen J, Chowirira BM;
XX WPI: 2001-607195/69.
DR
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., Lymphoma, leukemia,
PT and central nervous system injury
XX
XX Example 7, Page 170; 200pp; English.
PS
XX The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NIGO).
CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN
CC motif) or an amberzyme (cleaving RNA with an NCH triplet), a zinczyme
CC (cleaving RNA with a YG motif). The CD20-targeting nucleic acid is used
CC to cleave RNA of CD20 in the presence of a divalent cation that is used
CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
CC CD20 activity of the cell and treat a patient having a condition
CC associated with the level of CD20. The treatment may further comprise the
CC use of one or more therapies. In particular, the CD20 targeting
CC nucleic acid may be used to treat lymphoma, leukemia, B-cell
CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
CC low-grade or follicular NHL, lymphocytic leukaemia, HIV (human
CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
CC thrombocytopenia, and inflammatory arthropathy. The NIGO-targeting
CC nucleic acid is used to cleave RNA of the NIGO gene in the presence of a
CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
CC may be contacted with a cell to reduce NIGO activity of the cell and
CC treat a patient having a condition associated with the level of NIGO. The
CC treatment may further comprise the use of one or more therapies.
CC In particular, the NIGO-targeting nucleic acid may be used to treat
CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NIGO expression. The
CC present sequence is an enzymatic nucleic acid with trans-acting
CC inhibitory sequences (S- are substrate sequences, Rz- are enzymatic
CC nucleic acid and I- are inhibitory sequences).
XX
XX Sequence 27 BP; 4 A; 5 C; 10 G; 8 U; 0 other;
S0

Query Match 100.0%; Score 24; DB 23; Length 27;
Best Local Similarity 100.0%; Pred. NO. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctcgcaagcaccctatcagcagcagt 24
|||||
DB 25 CTCGCAAGCACCCTATCAGCAGCAGT 2

RESULT 27
AA705222
ID AAT05222 standard; DNA; 28 BP.
XX
XX AAT05222;
AC
XX 13-JUN-1996 (first entry)
DT
XX
DE Hepatitis C virus antisense oligonucleotide A312.
XX
XX Inhibition; expression; hepatitis C virus; HCV; non-A; non-B; RNA;
KW translation; in vivo; ex vivo; in vitro; treatment; prevention;
PI infection; antisense; non coding; region; NCR; core region; ss;
XX

XX
OS Synthetic.
XX
XX WO9530746-A1.
PN
XX 16-NOV-1995.
PD
XX 08-MAY-1995; 95MO-US05812.
PF
XX 10-MAY-1994; 94US-0240382.
PR
XX (GEHO) GEN HOSPITAL CORP.
PA
XX Wakita T, Wands JR;
PI
XX WPI: 1995-404113/51.
DR
XX New anti-sense hepatitis C virus oligo:nucleotide(s) - used for
PT inhibiting HCV RNA translation, for the treatment or prevention of
PT HCV infection
PT
XX
PS Claim 1; Page 29; 50pp; English.
XX
XX The present oligonucleotide (ON) inhibits the expression of
CC hepatitis C virus (HCV) RNA, specifically HCV type II and type III
CC protein synthesis is inhibited by 45% and 18%, respectively. The
CC ONs of the invention inhibit translation of HCV types I-V RNA in
CC vivo, ex vivo or in vitro, and can therefore be used to treat or
CC prevent HCV infection. The antisense ONs comprise 10-28
CC nucleotides complementary to the entire HCV 5'-non-coding and part
CC of the core region. The A or S in the ONs name denotes antisense
CC or sense, and the no. indicates the position of the 5'-end of the
CC ON. The ON was tested at 10 fold molar excess to HCV RNA.
XX
XX Sequence 28 BP; 8 A; 11 C; 5 G; 4 T; 0 other;
S0

Query Match 100.0%; Score 24; DB 16; Length 28;
Best Local Similarity 100.0%; Pred. NO. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctcgcaagcaccctatcagcagcagt 24
|||||
DB 2 ctcgcaagcaccctatcagcagcagt 25

RESULT 28
AA257757
ID AA257757 standard; DNA; 28 BP.
XX
XX AA257757;
AC
XX 05-APR-2000 (first entry)
DT
XX
DE Hepatitis C virus antisense inhibitor oligonucleotide A312.
XX
XX Hepatitis C virus; HCV; antisense oligonucleotide; hepatotropic; ss;
KW anti-inflammatory; translation inhibition; HCV infection; virucide.
XX
XX Hepatitis C virus.
OS
XX US6001990-A.
PN
XX 14-DEC-1999.
PD
XX 07-JUN-1995; 95US-0474700.
PF
XX 10-MAY-1994; 94US-0240382.
PR
XX (GEHO) GEN HOSPITAL CORP.
PA
XX Moradpour D, Wands JR, Wakita T;
PI
XX

DR WPI: 2000-104900/09.

XX Antisense oligonucleotide to Hepatitis C virus RNA, useful for treating
PT Hepatitis C virus infections -
XX

PS Claim 1: Column 23; 31pp; English.

XX This sequence is an antisense oligonucleotide that hybridises to
CC Hepatitis C virus (HCV) RNA, under physiological conditions. The
CC Invention relates to HCV antisense oligonucleotides, and also for a
CC vector comprising a nucleotide sequence which is transcribed in an animal
CC cell to generate an antisense oligonucleotide. The oligonucleotides have
CC virucide, hepatotropic and anti-inflammatory activity, and are useful for
CC treating HCV infection by inhibiting translation of type I-V HCV RNA.
CC Hepatitis C virus is a positive strand RNA virus, and is the major
CC causative agent of post-transfusion hepatitis. Persistent HCV infection
CC can lead to chronic hepatitis, cirrhosis, and hepatocellular carcinoma.
XX

SO Sequence 28 BP; 8 A; 11 C; 5 G; 4 T; 0 other:

Query Match

100.0%; Score 24; DB 21; Length 28;

Best Local Similarity 100.0%; Pred. No. 4.4e-05;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctcgaagcaccctatcagcagc 24

|||||

Db 2 ctcgaagcaccctatcagcagc 25

RESULT 29

AAQ53728

ID AAQ53728 standard; DNA; 30 BP.

XX AAQ53728;

DT 13-OCT-1994 (first entry)

DE Hepatitis C detection primer 2.

XX Key.

OS Synthetic.

XX JP06014800-A.

XX 25-JAN-1994.

XX 02-JUL-1992; 92JP-0197407.

XX 02-JUL-1992; 92JP-0197407.

XX (TOXJ) TOSOH CORP.

XX WPI: 1994-061488/08.

PT Detection of human hepatitis C virus - using primer contg. at
PT least 15 continuous bases

PS Claim 1: Page 1; 5pp; Japanese.

XX The primers (AAQ53727-728) are used to detect hepatitis C virus.
CC The method can amplify and detect specifically the nucleic acid
CC sequence originated from a trace amount of HCV contained in a
CC sample.

XX Sequence 30 BP; 8 A; 12 C; 6 G; 4 T; 0 other:

Query Match

100.0%; Score 24; DB 15; Length 30;

Best Local Similarity 100.0%; Pred. No. 4.4e-05;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctcgaagcaccctatcagcagc 24

|||||

Db 4 ctcgaagcaccctatcagcagc 27

RESULT 30

AAQ31158

ID AAQ31158 standard; DNA; 33 BP.

XX AAQ31158;

DT 24-MAR-1993 (first entry)

DE Probe 127 for genotyping analysis of HCV-1.

XX Hepatitis C virus: non-A, non-B hepatitis; polymerase chain reaction;
KW amplified solution phase nucleic acid sandwich assay;
KW genotyping analysis; capture probe; detection probe; ss.

XX Synthetic.

XX WO9219743-A.

XX 12-NOV-1992.

XX 08-MAY-1992; 92MO-US04036.

XX 08-MAY-1991; 91US-0697326.

XX (CHIR) CHIRON CORP.

XX Beall E, Cha T, Irvine B, Kolberg J, Urdea MS;

XX WPI: 1992-398869/48.

PT Compsn. comprising a non-hepatitis C virus-1 nucleotide sequence
PT related to HCV-1, useful for treating and detecting HCV-1
PT infections and as a vaccine

PS Claim 63; Page 140; 186pp; English.

CC A sandwich hybridisation assay can be used for HCV-1 genotyping
CC analysis. One example uses nucleotide sequences which correspond to
CC sequences in the C gene and the 5' UT region of HCV isolates as either
CC capture or detection probes. Probe 127 is preferably used as a capture
CC probe.

SO Sequence 33 BP; 8 A; 12 C; 9 G; 4 T; 0 other:

Query Match

100.0%; Score 24; DB 13; Length 33;

Best Local Similarity 100.0%; Pred. No. 4.4e-05;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctcgaagcaccctatcagcagc 24

|||||

Db 7 ctcgaagcaccctatcagcagc 30

RESULT 31

AAQ46464

ID AAQ46464 standard; DNA; 33 BP.

XX AAQ46464;

DT 13-DEC-1993 (first entry)

DE Hepatitis C virus RNA assay capture probe HCV.33.9.

XX Detection: HCV; reduced background signal; improved reproducibility;
KW hybridisation; 5'-untranslated region; C gene; ss.

XX Synthetic.

```

XX  MO9313224-A.
PN  08-JUL-1993.
XX
XX  22-DEC-1992; 92MO-US11343.
PF
XX  23-DEC-1991; 91US-0813338.
PR
XX  (CHIR ) CHIRON CORP.
PA
XX  Chang C, Running J, Sheridan P;
PI
XX  WPI; 1993-227338/28.
DR
XX  Immobilising nucleic acid probe on styrene, useful for HCV
PT  sequence detection - by using intermediate passively adsorbed
PT  polymer having functional gps. for covalently bonding to probe
PT  via its base-stable linkages
XX
XX  Example: Fig 3.1; 34pp; English.
XX
XX  The sequence is that of a synthetic capture probe which is
CC  complementary to nucleotide sequences in the hepatitis C virus
CC  C gene and the 5'-untranslated region. It may be used in an
CC  assay for the detection of HCV RNA.
XX
XX  Sequence 33 BP; 8 A; 12 C; 9 G; 4 T; 0 other;
SO

```

```

Query Match          100.0%; Score 24; DB 14; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY  1 ctcgcaagcaccctatcagcgagt 24
    ||||||||||||||||||||
DB  7 ctcgcaagcaccctatcagcgagt 30

```

```

RESULT 32
AAV07838
ID  AAV07838 standard; DNA; 33 BP.
XX
XX  AAV07838;
AC
XX  10-DEC-1998 (first entry)
DT
XX  HCV.33.9 amplifier probe.
DE
XX  Comb-type branched polynucleotide; amplification multimer; analyte;
KW  hybridisation assay; hepatitis c virus; HCV; amplifier probe; ss.
XX
XX  Synthetic.
OS  Hepatitis c virus.
XX
XX  US5710264-A.
PN
XX  20-JAN-1998.
PD
XX
XX  07-JUN-1995; 90US-0478085.
PE
XX  23-DEC-1991; 91US-0813588.
PR  27-JUL-1990; 90US-0558897.
PR  07-JUN-1995; 95US-0478085.
XX
XX  (CHIR ) CHIRON CORP.
PA
XX  Chang C, Fultz TJ, Horn T, Urdea MS, Warner B;
PI
XX  WPI; 1998-109872/10.
DR
XX
XX  New large comb-type branched polynucleotides - useful as
PT  amplification multimers in nucleic acid hybridisation assays

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XX  Example 6; Column 25; 33pp; English.
PS
XX

```

The invention relates to a large comb-type branched polynucleotide of formula: 3'-A-S-(S'-X')_mS'-5'; where X' is a branched site joined to -(R)n-S'-E-L; A = an oligonucleotide complementary to an analyte nucleic acid sequence; S = a first spacer segment of 1-50 linked monomers where each monomer is selected from nucleotides and a cleavable linker R; S' = a branching site spacer segment of 0-15 linked monomers where each of the monomers is selected from nucleotides and cleavable linker R; X' = a multifunctional nucleotide that provides a branch site; m = 1-100; S'' = a second spacer segment of 0-10 linked monomers where each of the monomers is selected from nucleotides and cleavable linker R; R = a cleavable linker molecule; n = 0 or 1; S''' = a third spacer segment of 0-10 linked monomers where each of the monomers is selected from nucleotides and cleavable linker R; E = an oligonucleotide segment of 5-10 nucleotides; L = an oligonucleotide containing 2-10 iterations of a nucleotide sequence complementary to a labelled nucleic acid probe. The invention also relates to a branched nucleic acid polymer. The polynucleotides are useful as amplification multimers in nucleic acid hybridisation assays used for genetic research, biomedical research and clinical diagnostics. Since the polynucleotide multimers include a large number (at least 20) iterations of a sequence that are available for specific hybridisation, they permit a greater degree of amplification and decrease the threshold level of a detectable analyte. The present sequence represents a hepatitis c virus (HCV) amplifier probe.

```

SQ  Sequence 33 BP; 8 A; 12 C; 9 G; 4 T; 0 other;

```

```

Query Match          100.0%; Score 24; DB 19; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY  1 ctcgcaagcaccctatcagcgagt 24
    ||||||||||||||||||||
DB  7 ctcgcaagcaccctatcagcgagt 30

```

```

RESULT 33
AAV83066
ID  AAV83066 standard; DNA; 33 BP.
XX
XX  AAV83066;
AC
XX  24-FEB-1999 (first entry)
DT
XX  Amplifier probe HCV.33.9.
DE
XX  Comb-type branched polynucleotide; amplifier probe;
KW  multifunctional nucleotide; pendant polynucleotide sidechain;
KW  hybridisation assay; amplification multimer; sandwich assay; ss.
XX
XX  Synthetic.
OS  Hepatitis C virus.
XX
XX  US5849481-A.
PN
XX  15-DEC-1998.
PD
XX
XX  05-JUN-1995; 95US-0470124.
PE
XX  23-DEC-1991; 91US-0813588.
PR  27-JUL-1990; 90US-0558897.
PR  05-JUN-1995; 95US-0470124.
XX
XX  (CHIR ) CHIRON CORP.
PA
XX  Chang C, Fultz TJ, Horn T, Urdea MS, Warner B;
PI
XX  WPI; 1999-069715/06.
DR
XX
XX  Improved nucleic acid hybridisation assays - using large comb-type
PT

```

```

PT polypeptide(s)
XX
XX Example 6; Column 24; 31pp; English.
CC
CC Oligonucleotides AAV83063-80 represent amplifier probes, used in a
CC sandwich hybridisation assay for Hepatitis C virus (HCV) DNA. The
CC polynucleotide amplification assay utilises the comb-type branched
CC comb-type branched polynucleotide comprises a polynucleotide
CC backbone having at least 15 multifunctional nucleotides each defining a
CC sidechain site and pendant polynucleotide sidechains extending from the
CC multifunctional nucleotides, each comprising iterations of a single
CC stranded oligonucleotide unit capable of binding specifically to a
CC second single-stranded polynucleotide sequence. The total number of
CC iterations in all sidechains is at least 20. The first single-stranded
CC polynucleotide sequence is a labelled polynucleotide, directly or
CC indirectly linked to a nucleic acid analyte. In the nucleic acid
CC hybridisation assay of the invention, the labelled nucleic acid probe
CC is hybridised to the branched polynucleotide via the second
CC single-stranded oligonucleotide unit. The comb-type branched
CC polynucleotides are used as amplification multimers in nucleic acid
CC hybridisation assays and other assays such as direct, indirect and
CC sandwich assays.
XX
SQ Sequence 33 BP; 8 A; 12 C; 9 G; 4 T; 0 other;

Query Match      100.0%; Score 24; DB 20; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcagcagc 24
    |||||||||||||||||||
DB 7 ctgcgaagcaccctatcagcagc 30

RESULT 34
AAV54436
ID AAV54436 standard; DNA; 40 BP.
XX
XX AAV54436;
AC
XX
XX 21-DEC-1998 (first entry)
DT
XX
XX Nucleotide sequence of HCV PCR primer 3.
DE
XX
XX Hepatitis C virus; HCV; PCR; primer; amplification; ss.
KM
XX
XX Synthetic.
OS
XX
XX JP10248579-A.
PN
XX
XX 22-SEP-1998.
PD
XX
XX 05-MAR-1997; 97JP-0067321.
PF
XX
XX 05-MAR-1997; 97JP-0067321.
PR
XX
XX (SRLS-) SRL KK.
PA (TOKR-) ZH TOKYO TO RINSHO IGAKU SOGO KENKYUSHO.
XX
XX WPI: 1998-560731/48.
DR
XX
XX
XX Determination of hepatitis C virus (HCV) gene - with real time
PT detective PCR and primer and probe used for determination
PS
XX
XX Claim 3; Page 6; 7pp; Japanese.
CC This is the nucleotide sequence of a Hepatitis C virus (HCV) PCR primer
CC used for amplification in the method of the invention. This is a useful
CC for the detection of the HCV gene.
XX
SQ Sequence 40 BP; 9 A; 17 C; 9 G; 5 T; 0 other;

```

```

Query Match      100.0%; Score 24; DB 19; Length 40;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcagcagc 24
    |||||||||||||||||||
DB 13 ctgcgaagcaccctatcagcagc 36

RESULT 35
AAQ98139
ID AAQ98139 standard; DNA; 53 BP.
XX
XX AAQ98139;
AC
XX
XX 05-FEB-1996 (first entry)
DT
XX
XX Control label extender probe used in an HCV sandwich hybridisation assay.
DE
XX
XX
XX Probe: nucleotide; solution phase sandwich hybridisation assay;
KM competitive; analyte binding sequence; background signal reduction;
KM comb body; Hepatitis C virus; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH misc_binding 21..53
FT /*tag= a
FT /note= "hybridises to target sequence"

W09516055-A1.
PN
XX
XX 15-JUN-1995.
PD
XX
XX 07-DEC-1994; 94WO-US14119.
PF
XX
XX 08-DEC-1993; 93US-0164388.
PR
XX
XX (CHIR ) CHIRON CORP.
PA
XX
XX Collins M, Fultz T, Urdea MS, Warner BD;
PI
XX
XX WPI: 1995-224335/29.
DR
XX
XX soln. phase sandwich hybridisation assays for nucleic acid(s) - with
PT capture extender molecules or competitive oligo:nucleotide(s) to
PT minimise background signal, increasing sensitivity and selectivity
PS
XX
XX Example 2; Page 43; 86pp; English.
XX
XX AAQ98125-098143 are control label extender probes (LEs) used in a
CC hepatitis C virus sandwich hybridisation assay used to demonstrate a
CC variation of a new improved method of a solution phase sandwich
CC hybridisation assay in which LEs are used with a capture probe (CP).
CC One label extender probe binds the target DNA and another binds to a
CC labelledprobe (LP).
CC The new method minimises background signals (caused by non-specific
CC hybridisation), this improves both sensitivity and selectivity of
CC the assay without increasing cost or time.
XX
SQ Sequence 53 BP; 12 A; 17 C; 15 G; 9 T; 0 other;

Query Match      100.0%; Score 24; DB 16; Length 53;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctgcgaagcaccctatcagcagc 24
    |||||||||||||||||||
DB 27 ctgcgaagcaccctatcagcagc 50

```

```
RESULT 36
AA098104
ID AA098104 standard; DNA; 53 BP.
XX
AC AA098104;
XX
DT 05-FEB-1996 (first entry)
XX
DE label extender probe used in an improved sandwich hybridisation assay.
XX
KW Probe; nucleotide; solution phase sandwich hybridisation assay;
XX competitive; analyte binding sequence; background signal reduction;
XX ss.
XX
OS Synthetic.
XX
PM W09516055-A1.
XX
PD 15-JUN-1995.
XX
PF 07-DEC-1994; 94MO-US14119.
XX
PR 08-DEC-1993; 93US-0164386.
XX
PA (CHIR ) CHIRON CORP.
XX
PI Collins M, Fultz T, Urdea MS, Warner BD;
XX
DR WPI; 1995-224335/29.
XX
PT Soln. phase sandwich hybridisation assays for nucleic acid(s) - with
XX capture extender molecules or competitive oligo;nucleotide(s) to
XX minimise background signal. Increasing sensitivity and selectivity
XX
PS Example 1; Page 33; 86pp; English.
XX
CC AA098100-098105 are label extender probes (LEs) used in a variation
XX of a new improved method of a solution phase sandwich hybridisation
XX assay in which LEs are used with a capture probe (CP). One label
XX extender probe binds the target DNA and another binds to a labelled
XX probe (LP).
XX CC The new method minimises background signals (caused by non-specific
XX hybridisation), this improves both sensitivity and selectivity of
XX the assay without increasing cost or time.
XX
SQ Sequence 53 BP; 12 A; 17 C; 15 G; 9 T; 0 other;

Query Match 100.0%; Score 24; DB 16; Length 53;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctcgcaagcaccctatcagcagc 24
    |||||||||||||||||||||
DB 27 ctcgcaagcaccctatcagcagc 50

RESULT 37
AA063223/C
ID AA063223 standard; RNA; 57 BP.
XX
AC AA063223;
XX
DT 13-JUN-1994 (first entry)
XX
DE Hepatitis C virus probe target region.
XX
KW Detection; HCV; 11:2 probe design.
XX
OS Hepatitis C virus.
XX
PM W09324656-A.
```

```
XX
PD 09-DEC-1993.
XX
PF 24-MAY-1993; 93MO-US04863.
XX
PR 29-MAY-1992; 92US-0891543.
XX
PA (ABBO ) ABBOTT LAB.
XX
PI Carrino JJ, Marshall RL, Sustachek JC;
XX
DR WPI; 1993-405844/50.
XX
PT Amplifying known RNA target for use in diagnosis of HIV and HCV
XX infection - by treating sample RNA with oligo-nucleotide probe,
XX extending probe by reverse transcription of target, dissociating
XX probe from target, hybridising 2nd probe with 1st, etc.
XX
PS Example 8; Page 26; 49pp; English.
XX
CC The sequence is that of the target region of probes (AA053257-053260)
XX used in the detection of hepatitis C virus (HCV) using a 11:2 probe
XX design. It corresponds to positions 246-302 of the 5' UTR of the
XX HPC8UMR sequence.
XX
SQ Sequence 57 BP; 9 A; 9 C; 23 G; 16 T; 0 other;

Query Match 100.0%; Score 24; DB 14; Length 57;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctcgcaagcaccctatcagcagc 24
    |||||||||||||||||||||
DB 57 ctcgcaagcaccctatcagcagc 34

RESULT 38
AA223543/C
ID AA223543 standard; DNA; 59 BP.
XX
AC AA223543;
XX
DT 21-DEC-1999 (first entry)
XX
DE HCV DNA fragment 2.
XX
KW Assay; amplification; hybridisation; probe; detection; viral; bacterial;
XX cellular; yeast; fungal; primer; ss.
XX
OS Hepatitis C virus.
XX
PM DE19814828-A1.
XX
PD 07-OCT-1999.
XX
PF 02-APR-1998; 98DE-1014828.
XX
PR 02-APR-1998; 98DE-1014828.
XX
PA (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI Kessler C, Haberland G, Batz H, Oerum H;
XX
DR WPI; 1999-552286/47.
XX
PT Nucleic acid amplification assay for detecting viral, bacterial,
XX cellular, yeast or fungal nucleic acids -
XX
PS Disclosure; Fig 7; 28pp; German.
XX
CC This invention describes a novel assay for a nucleic acid comprises:
XX (a) generating amplification products from a fragment of the nucleic
```

CC acid, (b) contacting the amplification products with a probe; and
 CC (c) detecting hybridization between the amplification product and the
 CC probe. The assay is useful for detection of viral, bacterial, cellular,
 CC yeast or fungal nucleic acids in human, animal, bacterial, plant, yeast
 CC or fungal samples, e.g. feces, smears, cell suspensions, cultures or
 CC tissue, cell or liquid biopsy samples. This sequence represents a
 CC fragment of the HCV genome used in the method of the invention.

XX
 SQ Sequence 59 BP; 9 A; 16 C; 21 G; 13 T; 0 other;

Query Match 100.0%; Score 24; DB 20; Length 59;
 Best Local Similarity 100.0%; Pred. No. 4.4e-05;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctcgcaagcaccctatcagcagc 24
 ||||||||||||||||||
 Db 26 CTCGCAGCACCCTATCAGCAGT 3

RESULT 39
 AA09795/C
 ID AA09795 standard; DNA; 59 BP.

AC AA09795;
 DT 26-NOV-1999 (first entry)

DE HCV DNA probe.

KM Probe; amplification; primer; reporter group; quencher group; PCR;
 KM amplicon; detection; ss.

OS Synthetic.
 OS Hepatitis C virus.

XX DE19814001-A1.

PD 30-SEP-1999.

PF 28-MAR-1998; 98DE-1014001.

PR 28-MAR-1998; 98DE-1014001.

PA (HOFF) ROCHE DIAGNOSTICS GMBH.

PI Kessler C, Habershausen G, Batz H, Orum H;

DR WPI: 1999-552213/47.

PT Fluorescent nucleic acid amplification assay, useful for detection of
 PT viral, bacterial, cellular, yeast or fungal nucleic acids

PS Disclosure: Fig 4; 16pp; German.

CC This invention describes a novel assay for a nucleic acid which comprises
 CC an amplification reaction using two non-overlapping primers, a polymerase
 CC with 5'-nuclease activity and a probe with reporter groups and a quencher
 CC groups that binds a region other than that bound by the primers. The
 CC reaction generates products of less than 100 nucleotides. The assay is
 CC useful for detection of viral, bacterial, cellular, yeast or fungal
 CC nucleic acids in human, animal, bacterial, plant, yeast or fungal
 CC samples, e.g. feces, smears, cell suspensions, cultures or tissue, cell
 CC or liquid biopsy samples. Compared with assays in which longer
 CC amplification products are generated, the assay can be performed more
 CC rapidly using shorter polymerase chain reaction (PCR) cycles, sensitivity
 CC may be increased due to reduced competition between the short
 CC counterstrand of the amplicon and the detector probe. Specificity may
 CC also be increased because of the increased relative length of sequence B
 CC compared with the total length of the amplicon and the differentiability
 CC of subtypes may be increased. In addition signal-to-noise ratios may be
 CC increased with the new method because short amplicons have reduced
 CC potential for nonspecific hybridization. In addition reproducibility may

CC be increased because small target regions on RNA genomes are less
 CC sensitive to RNA degradation, and the possibilities for secondary
 CC structure formation are reduced. This sequence represents a probe used to
 CC detect hepatitis C virus which is used to illustrate the method of the
 CC invention.

XX
 SQ Sequence 59 BP; 9 A; 16 C; 21 G; 13 T; 0 other;

Query Match 100.0%; Score 24; DB 20; Length 59;
 Best Local Similarity 100.0%; Pred. No. 4.4e-05;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctcgcaagcaccctatcagcagc 24
 ||||||||||||||||||
 Db 26 CTCGCAGCACCCTATCAGCAGT 3

RESULT 40
 AA098121
 ID AA098121 standard; DNA; 64 BP.

AC AA098121;

DT 05-FEB-1996 (first entry)

DE Label extender probe used in an HCV sandwich hybridisation assay.

KM Probe; nucleotide; solution phase sandwich hybridisation assay;

KM competitive; analyte binding sequence; background signal reduction;
 KM comb body; Hepatitis C virus; ss.

OS Synthetic.

OS Key Location/Qualifiers

FT misc_binding 17..49

FT /tag= a /note= "hybridises to target sequence"

PN W09516055-A1.

PD 15-JUN-1995.

PF 07-DEC-1994; 94WO-US14119.

PR 08-DEC-1993; 93US-0164388.

PA (CHIR) CHIRON CORP.

PI Collins M, Pultz T, Urdea MS, Warner BD;

DR WPI: 1995-22435/29.

PT Soln. phase sandwich hybridisation assays for nucleic acid(s) - with
 PT capture extender molecules or competitive oligo:nucleotide(s) to
 PT minimise background signal, increasing sensitivity and selectivity
 PS Example 2; Page 42; 86pp; English.

CC AA098118-098124 are label extender probes (LEs) used in a hepatitis C
 CC virus sandwich hybridisation assay used to demonstrate a variation
 CC of a new improved method of a solution phase sandwich hybridisation
 CC assay in which LEs are used with a capture probe (CP). One label
 CC extender probe binds the target DNA and another binds to a labelled
 CC probe (LP).

CC The new method minimises background signals (caused by non-specific
 CC hybridisation), this improves both sensitivity and selectivity of
 CC the assay without increasing cost or time.

SQ Sequence 64 BP; 18 A; 16 C; 17 G; 13 T; 0 other;

Query Match 100.0%; Score 24; DB 16; Length 64;

Best Local Similarity		100.0%	Pred. No.	4.4e-05					
Matches	24	Conservative	0	Mismatches	0	Indels	0	Gaps	0
QY	1	ctcgcaagcaccctatcagcagt	24						
Db	23	ctcgcaagcaccctatcagcagt	46						

RESULT	41
AAQ53257	
ID	AAQ53257 standard; DNA; 23 BP.

DT	13-JUN-1994 (first entry)
XX	
DE	Hepatitis C virus probe.
XX	

KW Detection; HCV; 11:2 probe design.

Synthetic.

Key	location/Qualifiers
modified_base	1
FT	/tag= a
FT	/note= "fluorescein labelled"
FT	

PN W09324656-A.

PD 09-DEC-1993.

PF 24-MAY-1993; 93WO-US04863.

PR 29-MAY-1992; 92US-0891543.

PA (ABBO) ABBOTT LAB.

PI Carrino JJ, Marshall RL, Sustachek JC;

DR WPI; 1993-405844/50.

PT Amplifying known RNA target or use in diagnosis of HIV and HCV
PT infection - by treating sample RNA with oligo-nucleotide probe,
PT extending probe by reverse transcription of target, dissociating
PT probe from target, hybridising 2nd probe with 1st, etc.

Example 8; page 25; 49pp; English.

CC The sequence is that of a probe which was used in the detection of
CC hepatitis C virus (HCV) using a 11:2 probe design. The probe is
CC specific for a part of the 5' UTR of the HPCvHMR sequence between
CC positions 246-302.

Sequence 23 BP; 6 A; 8 C; 5 G; 4 T; 0 other;

Query Match	95.8%	Score 23	DB 14	Length 23
Best Local Similarity	100.0%	Pred. No.	0.00017	
Matches 23	Conservative 0	Mismatches 0	Indels 0	Gaps 0

RESULT	42
AAQ37588	
ID	AAQ37588 standard; DNA; 29 BP.

DT 23-JUN-1993 (first entry)

DE HCV conserved region downstream primer/probe KY95, position 276-298
 XX
 XM Polymersae chain reaction; PCR; amplify; primer; probe; hepatitis C
 KM virus; HCV; conserved region; RNA; open reading frame; polyprotein;
 KM prototype; untranslated region; UTR, 5'UTR; conserved; replication;
 KM regulation; US; Japan; C9; ss.

OS Synthetic.

PN EP529493-A.

PD 03-MAR-1993.

PF 19-AUG-1992; 92EP-0114115.

PR 27-AUG-1991; 91DS-0751305

XX
XX
CROSSING THE FORD

XX
XX
Desibel
PV
vrouwe
vrou

XX 1003 060573 200
XX 1003 060573 200

XX DE

PT detecting hepatitis C virus strains Japan, US and C9

PS Claim 3; page 8; 43pp; English.

The sequences given in AA037569-96 are oligonucleotides which can be used as primers or probes which hybridise to the conserved region at the 5'-end of the hepatitis C virus (HCV) genome. HCV is a small RNA virus containing a small, positive sense, molecule of RNA about 10,000 nucleotides in length. The genome contains a single, long, open reading frame believed to translated in to a single, large polypeptide and subsequently processed. The open reading frame begins at nucleotide 343 (using the numbering system from the prototype virus) following an untranslated region (UTR) the 5' UTR sequence is relatively conserved and may be important in viral replication and regulation. The 5' end of the coding region is also conserved. These primer/probes can be used to identify different HCV isolates such as US, Japan and C9 (see also AA037597-601).

Sequence 29 BP; 8 A; 8 C; 8 G; 5 T; 0 other;

Query Match	95.8%;	Score 23;	DB 14;	Length 29;
Best Local Similarity	100.0%;	Pred. No. 0.00017;		
Matches 23;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

RESULT	43
AAAT64902	
ID	AAAT64902 standard; DNA; 29 BP
XX	
AC	AAAT64902;

DT 12-MAR-1998 (first entry)

DE Hepatitis C virus (HCV) oligonucleotide KY95.

KW Hepatitis C virus; reverse transcription; probe; PCR primer;

XX

OS Hepatitis C virus

PN EP787807-A2.

```

PD 06-AUG-1997.
XX 19-AUG-1992; 92EP-0065347.
XX 21-JUL-1992; 92US-0918844.
PR 27-AUG-1991; 91US-0751305.
XX
XX (HOEF ) HOFFMANN LA ROCHE & CO AG F.
XX Resnick RM, Young KKY;
XX WPI: 1997-387489/36.
XX
PT Oligo:nucleotide probes and primers for detecting hepatitis C virus
PT nucleic acid - from many different strains without loss of
PT specificity, allow single step reverse transcription and
PT amplification
XX
PS Claims 4 and 5; Page 8; 35pp; English.
XX
CC This oligonucleotide KY95 can be used as a probe for detecting
CC hepatitis C virus (HCV) nucleic acid from a Japanese or US prototype
CC strain as well as HCV C9 prototype strain. This oligonucleotide can
CC also be used as a primer for amplifying HCV nucleic acid. The sequence
CC of this oligonucleotide is contained in a specific region of HCV genomic
CC nucleic acid. The probe or the primer is preferably labelled. The probe
CC is used to detect HCV nucleic acid, preferably after this has been
CC amplified using the new primer in reverse transcription polymerase chain
CC reaction (RT-PCR), for both diagnostic and epidemiological applications.
CC The primer is effective for both reverse transcription and PCR,
CC eliminating the need to open the reaction tube during the procedure.
CC Amplification is effective (no need for a second round of PCR with nested
CC primers) and provides high sensitivity. The probe is directed to
CC conserved regions and so can detect many different strains without loss
CC of specificity.
XX
SQ Sequence 29 BP; 8 A; 8 C; 8 G; 5 T; 0 other;
XX
Query Match 95.8%; Score 23; DB 18; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 tcgcaagcacccctatcagcagct 24
| | | | | | | | | | | | | | | | | | | | |
DB 7 tcgcaagcacccctatcagcagct 29
.
RESULT 44
AA053259/C
ID AA053259 standard; DNA; 22 BP.
XX
XX AA053259;
XX 13-JUN-1994 (first entry)
XX Hepatitis C virus probe.
XX DE
XX Hepatitis C virus probe.
XX KM
XX Detection; HCV; 11:2 probe design.
XX OS
XX Synthetic.
XX
FH Key Location/Qualifiers
FH modified_base 22 /*tag= A
FT /note= "fluorescein labelled"
XX
XX WO9324656-A.
XX
XX 09-DEC-1993.
XX
XX 24-MAY-1993; 93WO-US04863.
XX

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PR      29-MAY-1992;      92US-0891543.
XX
XX      (ABBO ) ABBOTT LAB.
XX
PI      Carrino JJ, Marshall RL, Sustachek JC;
XX
DR      WPI; 1993-405844/50.
XX
XX      Amplifying known RNA target for use in diagnosis of HIV and HCV
PT      infection - by treating sample RNA with oligo-nucleotide probe,
PR      extending probe by reverse transcription of target, dissociating
XX      probe from target, hybridising 2nd probe with 1st, etc.
XX
PS      Example 8; Page 25; 49pp; English.
XX
CC      The sequence is that of a probe which was used in the detection of
CC      hepatitis C virus (HCV) using a 11:2 probe design. The probe is
CC      specific for a part of the 5' UTR of the HPCOHMR sequence between
CC      positions 246-302.
XX
SQ      Sequence 22 BP; 3 A; 4 C; 9 G; 6 T; 0 other;

Query Match      91.7%; Score 22; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 0 00067;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY      1 ctgcgaagcacccctatcagca 22
DB      22 ctgcgaagcacccctatcagca 1

RESULT 45
AAD25564
ID      AAD25564 standard; DNA; 23 BP.
XX
XX      AAD25564;
XX
DT      26-MAR-2002 (first entry)
XX
DE      HCV RNA 5' UTR amplifying PCR primer #2.
XX
KW      Hepatitis C virus; HCV; cytostatic; replication defective gene transfer;
KW      encapsidated RNA virus; gene therapy; cancer therapy; PCR primer; ss.
XX
OS      Hepatitis C virus.
XX
PN      WO200190302-A2.
XX
PD      29-NOV-2001.
XX
PF      10-MAY-2001; 2001WO-US15449.
XX
PR      24-MAY-2000; 2000US-206997P.
XX
PA      (FENG/) FENG Y.
XX      (TANG/) TANG H.
XX
PI      Feng Y, Tang H;
XX
XX      WPI; 2002-066766/09.
XX
XX      Producing encapsidated RNA virus by coexpressing RNA virus genomic
PT      sequence linked to bacteriophage promoter, and coding sequence for
PR      bacteriophage polymerase linked to poxvirus promoter in eukaryotic cell
XX      cytoplasm
XX
XX      Example 1; Page 30; 49pp; English.
XX
CC      The patent discloses methods to produce RNA viral sequences, recombinant
CC      RNA viruses, mutants of RNA viruses and RNA virus-derived vectors in
CC      cell culture and in vitro using non-viable, replication defective helper
CC      vaccinia recombinants. These methods generate RNA viral genomes and viral

```

CC particles in cell culture and in vitro independent of their natural
 CC replication pathways, bypassing the limitation of any cellular barriers.
 CC The invention also relates to a method for producing encapsidated RNA
 CC virus comprising coexpressing polypeptide coding sequences capable of
 CC forming capsid and packaging RNA viral genomic sequence linked to
 CC cell, a construct comprising RNA viral genomic sequence linked to
 CC bacteriophage promoter and transcription terminator and bacteriophage
 CC polymerase coding sequence, which is operably compatible with the
 CC promoter and is linked to poxvirus promoter. The methods are useful
 CC for producing infectious or non-infectious, replication-defective,
 CC encapsidated RNA viruses such as hepatitis virus comprising an RNA
 CC genome e.g. hepatitis C virus (HCV), immature hepatitis B virus or
 CC hepatitis A virus, lentivirus, rhinovirus, influenza virus, LCMV,
 CC arenavirus, parainfluenza virus, reovirus, rotavirus, astrovirus,
 CC filovirus, or coronavirus. They are preferably useful for producing
 CC encapsidated human immunodeficiency virus (HIV)-1, where the HIV-1
 CC lacks a Rev-response element (RRE) or an envelope sequence. Methods
 CC of the invention are also useful for producing replication defective
 CC gene transfer and gene therapy vectors, particularly to transfer nucleic
 CC acids to human cells in vivo and in vitro. The methods can be used for
 CC packaging therapeutic sequences as gene therapy vector preparations that
 CC are substantially free of helper virus and used as pharmaceuticals in
 CC e.g. gene replacement therapy, or cancer therapy. The present DNA
 CC sequence is a PCR primer which is used for amplifying the 5' untranslated
 CC region (UTR) of HCV RNA.
 CC
 XX

SQ Sequence 23 BP; 7 A; 9 C; 4 G; 3 T; 0 other;

Query Match 91.7%; Score 22; DB 24; Length 23;

Best Local Similarity 100.0%; Pred. No. 0.00068;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctgcgaagcaccctatcagca 22
 ||||||||||||||||||||
 Db 2 ctgcgaagcaccctatcagca 23

Search completed: August 26, 2002, 22:24:56
 Job time: 6235 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 20:41:01 ; Search time 450.99 Seconds
(without alignments)
91.368 Million cell updates/sec

Title: US-10-037-990A-1

Perfect score: 24
Sequence: 1 gcagaaagcgtctagccatgycgt 24

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 21

Total number of hits satisfying chosen parameters: 29

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database : N_Geneseq_032802:*

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2: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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13: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
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18: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SID5/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SID5/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SID5/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SID5/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	24	14	AAQ37573
2	24	100.0	24	16	AAQ75964
3	24	100.0	24	18	AAT64887
4	24	100.0	24	18	AAT93541
5	24	100.0	24	18	AAT87096
6	24	100.0	24	19	AAV18849
7	24	100.0	24	19	AAV15320
8	24	100.0	24	20	AAZ23536
9	24	100.0	24	20	AAZ09797

10	24	100.0	24	20	AAK78451
11	24	100.0	24	20	AAK23968
12	24	100.0	24	22	AAK19056
13	24	100.0	24	22	AAK25403
14	24	100.0	26	14	AAQ37574
15	24	100.0	26	18	AAT64888
16	24	100.0	26	18	AAT67193
17	24	100.0	26	19	AAV59058
18	24	100.0	26	22	AAH25413
19	24	100.0	77	22	AAK10490
20	23	95.8	37	16	AAK85920
21	23	95.8	37	16	AAQ75035
22	23	95.8	58	16	AAQ75033
23	21	87.5	21	14	AAQ52817
24	21	87.5	21	19	AAV70448
25	21	87.5	21	21	AAK72990
26	21	87.5	21	22	AAH79078
27	21	87.5	21	24	ABA01127
28	21	87.5	24	22	AAH79081
29	21	87.5	25	16	AAQ98291

ALIGNMENTS

```
RESULT 1
AAQ37573
ID AAQ37573 standard: DNA; 24 BP.
XX
AC AAQ37573:
XX
DT 23-JUN-1993 (first entry)
XX
DE HCV conserved region upstream primer/probe KY80, position 56-79.
XX
KW Polymerase chain reaction; PCR; amplify; primer; probe; hepatitis C;
KW virus; HCV; conserved region; RNA; open reading frame; polypeptide;
KW prototype; untranslated region; UTR; 5'UTR; conserved; replication;
KW regulation; US; Japan; C9; ss.
XX
OS Synthetic.
XX
PN EP529493-A.
XX
PD 03-MAR-1993.
XX
PF 19-AUG-1992; 92BP-0114115.
XX
PR 27-AUG-1991; 91US-0751305.
PR 21-JUL-1992; 92US-0918844.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Resnick RM, Young KKY.
XX
DR WPI; 1993-068572/09.
XX
PT Compens. comprising oligo:nucleotide probe-primer - used for
PT detecting hepatitis C virus strains Japan, US and C9
XX
PS Claim 4; Page 7; 43pp; English.
XX
XX
The sequences given in AAQ37569-96 are oligonucleotides which can be
used as primers or probes which hybridise to the conserved region at
the 5'-end of the hepatitis C virus (HCV) genome. HCV is a small
RNA virus containing a small, positive sense, molecule of RNA about
10,000 nucleotides in length. The genome contains a single, long,
open reading frame believed to translated in to a single, large
polyprotein and subsequently processed. The open reading frame
begins at nucleotide 343 (using the numbering system from the
prototype virus) following an untranslated region (UTR) the 5'UTR
sequence is relatively conserved and may be important in viral
replication and regulation. The 5' end of the coding region is also
```

CC conserved. These primer/probes can be used to identify different HCV
CC isolates such as US, Japan and C9 (see also AAQ37597-601).
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaaagcgtctagccatgagcgt 24
|||||
DB 1 gcagaaagcgtctagccatgagcgt 24

RESULT 2

AAQ79964
ID AAQ79964 standard; DNA; 24 BP.

XX
AC AAQ79964;

DT 01-AUG-1995 (first entry)

XX
XX Primer KY90 for HCV RNA.

DE Primer: PCR; polymerase chain reaction; amplification;

KW RNA detection; reverse transcription; hepatitis C virus; HCV;

XX
OS Synthetic.

XX
PN EP632134-A.

XX
PD 04-JAN-1995.

XX
PF 20-JUN-1994; 94EP-0109468.

XX
PR 01-JUL-1993; 93US-0086483.

XX
PA (HOPE) HOFFMANN LA ROCHE & CO AG F.

XX
PI Gelfand DH, Myers TW, Sigua CL;

DR WPI; 1995-037815/06.

XX
PT Improved amplification method for target RNA - using buffering

XX
PT agent which buffers both pH and divalent cation concn.

PS Example 6; Page 22; 37pp; English.

XX
CC The primers given in AAQ79963-64 were used to amplify HCV templates

CC for use in a novel method of RNA amplification involving

CC high-temp. reverse transcription and PCR.
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaaagcgtctagccatgagcgt 24
|||||
DB 1 gcagaaagcgtctagccatgagcgt 24

RESULT 3

AA764887
ID AAT64887 standard; DNA; 24 BP.

XX
AC AAT64887;

XX
DT 12-MAR-1998 (first entry)

XX
DE Hepatitis C virus (HCV) oligonucleotide KY80.

XX
KW Hepatitis C virus; reverse transcription; probe; PCR primer;

XX
KW detection; ss.

OS Synthetic.

OS Hepatitis C virus.

XX
PN EP787807-A2.

XX
PD 06-AUG-1997.

XX
PF 19-AUG-1992; 92EP-0065347.

XX
PR 21-JUL-1992; 92US-0918844.

XX
PR 27-AUG-1991; 91US-0751305.

XX
PA (HOPE) HOFFMANN LA ROCHE & CO AG F.

XX
PI Resnick RM, Young KKY;

DR WPI; 1997-387489/36.

XX
PT Oligo:nucleotide probes and primers for detecting hepatitis C virus

PT nucleic acid - from many different strains without loss of

PT specificity, allow single step reverse transcription and

PT amplification
XX
PS Claims 2 and 5; Page 7; 35pp; English.

XX
CC This oligonucleotide KY80 can be used as a probe for detecting

CC hepatitis C virus (HCV) nucleic acid from a Japanese or US prototype

CC strain. This oligonucleotide can also be used as a primer for amplifying

CC HCV nucleic acid. This primer is capable of amplifying HCV C9 prototype

CC strains also. The sequence of this oligonucleotide is contained in a

CC specific region of HCV genomic nucleic acid. The probe or the primer

CC is preferably labelled. The probe is used to detect HCV nucleic acid,

CC preferably after this has been amplified using the new primer in reverse

CC transcription polymerase chain reaction (RT-PCR), for both diagnostic and

CC epidemiological applications. The primer is effective for both reverse

CC transcription and PCR, eliminating the need to open the reaction tube

CC during the procedure. Amplification is effective (no need for a second

CC round of PCR with nested primers) and provides high sensitivity. The

CC probe is directed to conserved regions and so can detect many different

CC strains without loss of specificity.
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 18; Length 24;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaaagcgtctagccatgagcgt 24
|||||
DB 1 gcagaaagcgtctagccatgagcgt 24

RESULT 4

AA793541
ID AAT93541 standard; DNA; 24 BP.

XX
AC AAT93541;

XX
DT 19-FEB-1998 (first entry)

XX
DE Sense primer KY80 for amplification of HCV RNA.

XX
KW Armoured RNA: bacteriophage MS2; RT-PCR: ribonuclease; recombinant;

XX
KW Human immunodeficiency virus; HIV; Hepatitis C Virus; HCV; viral RNA;

XX
KW detection; quantification standard; maturation protein; coat protein;

XX
KW PCR primer; QS RNA; reverse transcriptase-PCR; ss.

PA	(HYDS) HRI RES INC.
XX	
PI	Lin L;
XX	
DR	WPI; 1997-401849/37.
XX	
PT	Preparation of RNA samples from plasma - by alcohol precipitation
PT	after lysis with guanidinium thiocyanate
XX	
PS	Disclosure; Column 47; 60pp; English.
XX	
CC	Primer KY80 (AAAT87096) and primer KY78 (AAT87095) were used for the
CC	PCR amplification of a 305 bp hepatitis C virus gene product (see
CC	AAAT87088). A claimed method for preparing RNA samples comprises: (a)
CC	mixing plasma with an aqueous buffer solution containing guanidinium
CC	thiocyanate and beta-mercaptoethanol; (b) heating the mixture; (c)
CC	adding an equal volume of an alcohol to precipitate RNA; and (d)
CC	recovering the RNA. The method can be used to prepare RNA samples
CC	for subsequent amplification, especially for detecting pathogens,
CC	e.g. hepatitis C virus or HIV. Compared with the known "Isoquick"
CC	and "RNezol" methods, the method uses fewer tubes (just one).
CC	requires fewer steps, takes less time and produces no toxic waste.
XX	
SQ	Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other:
Query Match	100.0%; Score 24; DB 18; Length 24;
Best Local Similarity	100.0%; Pred. NO. 7e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 gcagaaagcgctacgcatgcgt 24
DG	1 gcagaaagcgctacgcatgcgt 24
RESULT 6	
ID	AAV18849 standard; DNA; 24 BP.
XX	
AC	AAV18849;
XX	
DT	11-JUN-1998 (first entry)
XX	
DE	Primer KY80 for HCV DNA.
XX	
KM	PCR primer; HCV; nucleic acid standard; Armored RNA; ss.
XX	
OS	Synthetic.
OS	Hepatitis virus.
XX	
PN	MO9800547-A1.
XX	
PD	08-JAN-1998.
XX	
PE	02-JUL-1997; 97WO-US12551.
XX	
PR	24-JUN-1997; 97US-0881571.
PR	03-JUL-1996; 96US-0021145.
PR	03-JUL-1996; 96US-0675153.
XX	
PA	(AMBI-) AMBION INC.
PA	(CENE-) CENTRON DIAGNOSTICS LLC.
XX	
PI	Dubois DB, Pasloske BL, Winkler MM;
XX	
DR	WPI; 1998-086972/08.
XX	
PT	Ribonuclease resistant RNA molecules and their production - useful
PT	as standards in quantitative PCR for pathogens, e.g HIV-1, HIV-2 and
XX	
HCY	
XX	
SS	Example 5; Page 41; 134pp; English.
XX	

QY 1 gcagaaagcgtcttagccatggcgt 24

probe; amplification; primer; reporter group; quencher group; PCR; amplification; detection; ss

```
XX OS Synthetic.
OS Hepatitis C virus.
XX PN DE19814001-A1.
XX PD 30-SEP-1999.
XX PF 28-MAR-1998; 98DE-1014001.
XX PR 28-MAR-1998; 98DE-1014001.
XX PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX PI Kessler C, Habershausen G, Batz H, Orum H;
XX WPI; 1999-552213/47.
XX PT Fluorescent nucleic acid amplification assay, useful for detection of
XX viral, bacterial, cellular, yeast or fungal nucleic acids
XX PS Example 1; Page 19; 16pp; German.
XX CC This invention describes a novel assay for a nucleic acid which comprises
CC an amplification reaction using two non-overlapping primers, a polymerase
CC with 5'-nuclease activity and a probe with reporter groups and quencher
CC groups that binds a region other than that bound by the primers. The
CC reaction generates products of less than 100 nucleotides. The assay is
CC useful for detection of viral, bacterial, cellular, yeast or fungal
CC nucleic acids in human, animal, bacterial, plant, yeast or fungal
CC samples, e.g. feces, smears, cell suspensions, cultures or tissue, cell
CC or liquid biopsy samples. Compared with assays in which longer
CC amplification products are generated, the assay can be performed more
CC rapidly using shorter polymerase chain reaction (PCR) cycles, sensitivity
CC may be increased due to reduced competition between the short
CC counterstrand of the amplicon and the detector probe. Specificity may
CC also be increased because of the increased relative length of sequence B
CC compared with the total length of the amplicon and the differentiability
CC of subtypes may be increased. In addition signal-to-noise ratios may be
CC increased with the new method because short amplicons have reduced
CC potential for nonspecific hybridization. In addition reproducibility may
CC be increased because small target regions on RNA genomes are less
CC sensitive to RNA degradation, and the possibilities for secondary
CC structure formation are reduced. This sequence represents a PCR primer
CC used in the amplification of a region of HCV which is used to illustrate
CC the method of the invention.
XX SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaaagcgtctagccatgcgt 24
   ||||||||||||||||||||
DT 1 gcagaaagcgtctagccatgcgt 24
Db 1 gcagaaagcgtctagccatgcgt 24

RESULT 10
AAK78451
ID AAK78451 standard; DNA; 24 BP.
XX AC AAK78451;
XX DT 26-AUG-1999 (first entry)
XX DE HCV PCR primer 1.
XX RNA standard; HCV; detection; gag gene; cerebrospinal fluid; PCR primer;
XX ribonuclease resistant; encapsulation; viral; HIV-1; HIV-2; HCV;
XX HTLV-1; HTLV-2; hepatitis G; enterovirus; blood-borne pathogen; ss.
XX
```

```
OS OS Synthetic.
OS Hepatitis C virus.
XX PN US5919625-A.
XX PD 06-JUL-1999.
XX PF 29-APR-1997; 97US-0841252.
XX PR 03-JUL-1996; 96US-0675153.
XX PR 29-APR-1997; 97US-0841252.
XX PA (AMBI-) AMBION INC.
XX PA (CENDE-) CENETRON DIAGNOSTICS LLC.
XX PI Dubois DB, Pasloske BL, Winkler MM;
XX WPI; 1999-394617/33.
XX PT Ribonuclease resistant viral RNA standards
XX PS Example V; Column 31-32; 22pp; English.
XX CC This invention describes the construction of novel RNA standards for the
XX quantification of human immunodeficiency virus (HIV) and hepatitis C
XX virus (HCV) from e.g. cerebrospinal fluids. The method involves (1)
XX obtaining a sample to be analysed; (2) obtaining a ribonuclease resistant
XX RNA standard, encapsulated in a bacteriophage viral coat protein, which
XX comprises an RNA segment having a segment encoding a sequence that serves
XX as a standard in detection or quantification of the RNA of interest;
XX (3) mixing the sample with the standard; (4) isolating RNA from the
XX mixture; and (5) assaying for the presence of the RNA. The method is
XX used for the detection or quantification of HIV-1, HIV-2, HCV, HTLV-1,
XX HTLV-2, hepatitis G, an enterovirus, or a blood-borne pathogen. This
XX sequence represents a PCR primer used to amplify a region of the
XX Hepatitis C genome which is used in the method of the invention.
XX SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaaagcgtctagccatgcgt 24
   ||||||||||||||||||||
DT 1 gcagaaagcgtctagccatgcgt 24
Db 1 gcagaaagcgtctagccatgcgt 24

RESULT 11
AAK23968
ID AAK23968 standard; DNA; 24 BP.
XX AC AAK23968;
XX DT 28-JUN-1999 (first entry)
XX DE PCR primer KY80.
XX Amplification; medical; forensic; diagnosis; food analysis; blood;
XX environmental analysis; plant protection; veterinary medicine;
XX human immune deficiency virus; hepatitis B; hepatitis C; Chlamydia;
XX screening; PCR primer; detection; probe; ss.
XX OS Synthetic.
XX PN DE19748690-A1.
XX PD 06-MAY-1999.
XX PR 04-NOV-1997; 97DE-1048690.
XX PR 04-NOV-1997; 97DE-1048690.
XX
```

DR	WPI; 2001-611396/70.
XX	
PT	Simultaneous detection
PT	and viruses by

PT and viruses by specific nucleic acid amplification -
 f1 simultaneous detection of biological entities such as bacteria, fungi
 XX
 PS
 Disclosure: Page 31, 55pp; English.

PS Disclosure; Page 31; 55pp; English
XX

The invention relates to a method and apparatus for the simultaneous detection of multiple biological entities such as bacteria, fungi and viruses by specific nucleic acid amplification. The invention also relates to a kit for simultaneous detection of biological entities. The kit is employed for detecting blood-borne pathogens, associated with a variety of infectious diseases such as respiratory and sexually transmitted diseases. The methods and apparatus are used for the simultaneous detection of biological entities present in biological and environment samples. In particular, they are used for monitoring diseases caused by microorganisms associated with a respiratory or sexually transmitted disease such as a bacterium (*Staphylococcus*, *Pneumococcus*, *Gonococcus*, *Haemophilus*, *Bacteroides*, *Escherichia* or *Salmonella*), virus (DNA or RNA virus, such as adenovirus, adenoviricella or *Salmonella*), HIV, HEV, HCV or TTV), fungus (*Aspergillus fumigatus*, *Blastomycosis*, dermatitis, *Candida albicans*) or protozoa (*Entamoeba histolytica*). The present sequence is a PCR primer used for amplifying Hepatitis viral DNA.

Sequence 24 BP: 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match	Score 24;	DB 22;	Length 24;
100.08;			
100.08;			
Best Local Similarity			

QY	Db
1 gcagaaagcgtctagccatgycgt 24	1 gcagaaagcgtctagccatgycgt 24

ID	AAH25403	standard; DNA; 24 BP
yy	AAH25403	

DT 22-AUG-2001 (first entry)
XY

PCR primer used to amplify a HCV DNA fragment

magnetic glass particle; nucleic acid purification; PCR primer; ss.

Hepatitis C virus.

PN WO200137291-A1.

PD 25-MAY-2001.
XX

1/-NOV-2000; 2000WO-EP11459.

PR	1/-NOV-1999;	99EP-0122853.
PR	13-MAY-2000;	2000ED-0110155.

XX
XX
(HOFF) BOCHER DIAGNOSTIC CODE:

(HOFF) ROCHE DIAGNOSTICS GMBH.

Weindel K, Riedling M, Geiger A;

WPI; 2001-381247/40.

Novel composition of magnetic glass particles for purification of DNA

Example 7; Page 94; 105pp; English.

The specification describes a composition of magnetic glass particles, which contain at least one magnetic object with a mean diameter between

CC 5-500 nm. The composition is useful for the purification of nucleic acids. The composition can be used to process large quantities of CC nucleic acid samples, because it does not involve the particles being CC centrifuged or the fluids being drawn through glass fiber filters. CC PCR primers AAH25403-04 were used to amplify HCV DNA fragments. The CC amplified fragment can be purified using the method of the invention. XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 22; Length 24;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaagcgtctagccatgagcgt 24
|||||
DB 1 gcagaagcgtctagccatgagcgt 24

RESULT 14

AA037574
ID AA037574 standard; DNA; 26 BP.

AC AA037574;

DT 23-JUN-1993 (first entry)

DE HCV conserved region upstream primer/probe KY144, position 54-79.

KM Polymerase chain reaction; PCR; amplify; primer; probe; hepatitis C;
KM virus; HCV; conserved region; RNA; open reading frame; polyprotein;
KM prototype; untranslated region; UTR; 5'UTR; conserved; replication;
KM regulation; US; Japan; C9; ss.

OS Synthetic.

FN EP529493-A.

PD 03-MAR-1993.

PF 19-AUG-1992; 92EP-0114115.

PR 27-AUG-1991; 91US-0751305.

PR 21-JUL-1992; 92US-0918844.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

PI Resnick RM, Young KKY;

DR WPI; 1993-068572/09.

PT Compsn. comprising oligo:nucleotide probe-primer - used for
PT detecting hepatitis C virus strains Japan, US and C9

PS Claim 4; Page 7; 43pp; English.

CC The sequences given in AA037569-96 are oligonucleotides which can be
CC used as primers or probes which hybridise to the conserved region at
CC the 5' end of the hepatitis C virus (HCV) genome. HCV is a small
CC RNA virus containing a small, positive sense, molecule of RNA about
CC 10,000 nucleotides in length. The genome contains a single, long,
CC open reading frame believed to translated in to a single, large
CC polyprotein and subsequently processed. The open reading frame
CC begins at nucleotide 343 (using the numbering system from the
CC prototype virus) following an untranslated region (UTR) the 5'UTR
CC sequence is relatively conserved and may be important in viral
CC replication and regulation. The 5' end of the coding region is also
CC conserved. These primer/probes can be used to identify different HCV
CC isolates such as US, Japan and C9 (see also AA037597-601).

SQ Sequence 26 BP; 7 A; 7 C; 8 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 14; Length 26;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaagcgtctagccatgagcgt 24
|||||
DB 3 gcagaagcgtctagccatgagcgt 26

RESULT 15

AA64888
ID AA64888 standard; DNA; 26 BP.

AC AA64888;

DT 12-MAR-1998 (first entry)

DE Hepatitis C virus (HCV) oligonucleotide KY144.

KM Hepatitis C virus; reverse transcription; probe; PCR primer;
KM detection; ss.

OS Synthetic.

OS Hepatitis C virus.

PN EP787807-A2.

PD 06-AUG-1997.

PF 19-AUG-1992; 92EP-0065347.

PR 21-JUL-1992; 92US-0918844.

PR 27-AUG-1991; 91US-0751305.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

PI Resnick RM, Young KKY;

DR WPI; 1997-387489/36.

PT Oligo:nucleotide probes and primers for detecting hepatitis C virus
PT nucleic acid - from many different strains without loss of
PT specificity, allow single step reverse transcription and
PT amplification

PS Claims 2 and 5; Page 7; 35pp; English.

CC This oligonucleotide KY144 can be used as a probe for detecting
CC hepatitis C virus (HCV) nucleic acid from a Japanese or US prototype
CC strain. This oligonucleotide can also be used as a primer for amplifying
CC HCV nucleic acid. This primer is also capable of amplifying a HCV C9
CC prototype strain. The sequence of this oligonucleotide is contained
CC in a specific region of HCV genomic nucleic acid. The probe or the primer
CC is preferably labelled. The probe is used to detect HCV nucleic acid,
CC preferably after this has been amplified using the new primer in reverse
CC transcription polymerase chain reaction (RT-PCR), for both diagnostic and
CC epidemiological applications. The primer is effective for both reverse
CC transcription and PCR, eliminating the need to open the reaction tube
CC during the procedure. Amplification is effective (no need for a second
CC round of PCR with nested primers) and provides high sensitivity. The
CC probe is directed to conserved regions and so can detect many different
CC strains without loss of specificity.

SQ Sequence 26 BP; 7 A; 7 C; 8 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 18; Length 26;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaagcgtctagccatgagcgt 24
|||||
DB 3 gcagaagcgtctagccatgagcgt 26

```
RESULT 16
AA67193
ID AAT67193 standard; DNA: 26 BP.
XX
AC AAT67193:
XX
DT 13-FEB-1998 (first entry)
XX
DE Hepatitis C virus (HCV) RNA amplification primer ST280A.
XX
KW Hepatitis C virus; HCV; ST280A; reverse transcription PCR; RT-PCR;
XX PCR primer; ss.
XX
OS Synthetic.
XX
PN EP776981-A2.
XX
PD 04-JUN-1997.
XX
PF 21-NOV-1996; 96EP-0118704.
XX
PR 29-NOV-1995; 95US-0007739.
XX
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI Tsang SY;
XX
DR WPI: 1997-291296/27.
XX
PT Oligonucleotide primers for hepatitis C virus RNA amplification
XX by polymerase chain reaction
XX
PS Claim 1; Page 11; 16pp; English.
XX
CC This upstream primer ST280A is used in the amplification of the
CC Hepatitis C virus (HCV) RNA by reverse transcription PCR. This is used
CC to amplify a 250 base pair product from the 5' untranslated region of
CC the HCV genome. This can be used to detect HCV in a sample with increased
CC sensitivity. Amplification of HCV nucleic acid using this primer is up to
CC 100 times more efficient than amplification with prior art primers.
XX
SQ Sequence 26 BP; 7 A; 6 C; 8 G; 5 T; 0 other:

Query Match 100.0%; Score 24; DB 18; Length 26;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaaagcgtctagcattgagcgt 24
DB 1 gcagaaagcgtctagcattgagcgt 24

RESULT 17
AAV59058
ID AAV59058 standard; DNA: 26 BP.
XX
AC AAV59058:
XX
DT 07-JAN-1999 (first entry)
XX
DE Primer ST280A for HCV fragment.
XX
KW PCR primer; HCV; nucleic acid amplification; ss.
XX
OS Synthetic.
XX
OS Human cytomegalovirus.
XX
FH key Location/Qualifiers
FT modified_base 26
FT /*tag= a
```

```
FT /note= "optionally benzylated, methylated, or
FT nitrobenzylated"
XX
PN EP866071-A2.
XX
PD 23-SEP-1998.
XX
PF 12-MAR-1998; 98EP-0104461.
XX
PR 20-MAR-1997; 97US-0041127.
XX
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI Will SG, Young KKY;
XX
DR WPI: 1998-482929/42.
XX
PT Oligo-nucleotide(s) containing N-substituted nucleotide - useful as
XX primers for nucleic acid amplification
XX
PS Example 6; Page 16; 38pp; English.
XX
CC This sequence represents a primer for a fragment of HCV, and is an
CC example of an oligonucleotide of the invention. The oligonucleotides of
CC the invention are of the formula 5'-S1-Nu-3' or 5'-S1-Nu-S2-3', where
CC S1 is a sequence of 5-50 nucleotides; S2 is a sequence of 1-3
CC nucleotides; and Nu is a nucleotide with a purine or pyrimidine base
CC having an exocyclic amino group substituted by CHR1R2; R1, R2 are H,
CC 1-10C alkyl, alkoxy, optionally substituted phenyl, phenoxy or optionally
CC substituted naphthyl. The oligonucleotides are useful as primers for
CC nucleic acid amplification, preferably by polymerase chain reaction. Use
CC of the modified primers reduces non-specific amplification, especially
CC primer dimer formation, with a concomitant increase in the yield of the
CC intended target.
XX
SQ Sequence 26 BP; 7 A; 6 C; 8 G; 5 T; 0 other:

Query Match 100.0%; Score 24; DB 19; Length 26;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaaagcgtctagcattgagcgt 24
DB 1 gcagaaagcgtctagcattgagcgt 24

RESULT 18
AAH25413
ID AAH25413 standard; DNA: 26 BP.
XX
AC AAH25413:
XX
DT 22-AUG-2001 (first entry)
XX
DE Forward PCR primer used to amplify a HCV DNA fragment.
XX
KW Magnetic glass particle; nucleic acid purification; PCR primer; ss.
XX
OS Hepatitis C virus.
XX
FH key Location/Qualifiers
FT modified_base 26
FT /*tag= a
FT /note= "derivatization with a p-(t-butyl)benzyl-residue"
XX
PN WO200137291-A1.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-EP11459.
XX
PR 17-NOV-1999; 99EP-0122853.
```

```
PR 12-MAY-2000; 2000EP-0110165.
XX
XX (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
XX Weindel K, Riedling M, Geiger A;
XX
XX WPI; 2001-381247/40.
XX
XX
XX Novel composition of magnetic glass particles for purification of DNA
XX or RNA in automated processes
XX
XX Example 7, Page 98; 105pp; English.
XX
XX The specification describes a composition of magnetic glass particles,
XX which contain at least one magnetic object with a mean diameter between
XX 5-500 nm. The composition is useful for the purification of nucleic
XX acids. The composition can be used to process large quantities of
XX nucleic acid samples, because it does not involve the particles being
XX centrifuged or the fluids being drawn through glass fiber filters.
XX PCR primers AAH25413-14 were used to amplify HCV DNA fragments. The
XX amplified fragment can be purified using the method of the invention.
XX
XX
XX Sequence 26 BP; 7 A; 6 C; 8 G; 5 T; 0 other;

Query Match      100.0%; Score 24; DB 22; Length 26;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaaagcgtctagccatgcgcgt 24
   |||||||||:|||||:|||||
DB 1 gcagaaagcgtctagccatgcgcgt 24

RESULT 19
AAS10490
ID AAS10490 standard; RNA; 77 BP.
XX
XX AAS10490;
AC
XX
XX 24-OCT-2001 (first entry)
DE
XX HCV 5'-UTR domain II EMSA RNA probe.
XX
XX HCV 5'-UTR; minimal IRES; mIRES; internal ribosome entry site; eIF3;
XX eukaryotic initiation factor 3; HCV translation initiation; antiviral;
XX RNA electrophoretic gel mobility shift assay; EMSA; ss.
XX
XX Hepatitis C virus strain Ia M67463.
XX
XX
XX Key Location/Qualifiers
XX misc_binding 1..5
XX /tag= a
XX /bound_moiety= "Forms double stranded region with
XX bases 73-77"
XX
XX stem_loop 8..22
XX /tag= c
XX /note= "Designated as Ila"
XX
XX misc_binding 23..28
XX /tag= b
XX /bound_moiety= "Forms double stranded region with
XX bases 60-55"
XX
XX stem_loop 32..50
XX /tag= c
XX /note= "Designated as IIB"
XX
XX misc_binding 55..60
XX /tag= d
XX /bound_moiety= "Forms double stranded region with
XX bases 28-23"
XX
XX misc_binding 73..77
XX /tag= e
XX /bound_moiety= "Forms double stranded region with
XX bases 5-1"
```

```
XX
XX WO200144266-A2.
XX
XX
XX 21-JUN-2001.
XX
XX
XX 18-DEC-2000; 2000WO-GB04862.
XX
XX
XX 16-DEC-1999; 99GB-0029820.
XX
XX 22-DEC-1999; 99US-0171804.
XX
XX (RIBO-) RIBOTARGETS LTD.
XX
XX
XX Karn J, Walker S;
XX
XX WPI; 2001-465050/50.
XX
XX Nucleotide sequences derived from Hepatitis C virus, useful for
XX identifying candidate antiviral compounds -
XX
XX Disclosure; Fig 5E; 48pp; English.
XX
XX The present sequence represents Hepatitis C virus (HCV) 5'-UTR
XX domain II RNA probe used in a RNA electrophoretic gel mobility
XX shift assay (EMSA). The present sequence is described in an
XX invention relating to a novel compound comprising nucleotide sequences
XX capable of annealing and which is derived from a 5'-untranslated
XX region (UTR) of HCV which is essential for binding of eIF3 (eukaryotic
XX initiation factor 3). The invention particularly relates to a
XX sub-region of the HCV 5'-UTR referred to as the minimal internal
XX ribosome entry site (mIRES) which can be used to identify drugs which
XX inhibit HCV translation initiation. The compounds of the invention may
XX be used to screen for potential HCV antiviral compounds. Assays based
XX on the mIRES enable potential antivirals to be screened in a cheaper
XX and easier way. It allows rapid assaying with a small volume of
XX material and are suitable to parallel processing.
XX
XX
XX Sequence 77 BP; 16 A; 20 C; 23 G; 18 U; 0 other;

Query Match      100.0%; Score 24; DB 22; Length 77;
Best Local Similarity 83.3%; Pred. No. 6.9e-05;
Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaaagcgtctagccatgcgcgt 24
   |||||||||:|||||:|||||
DB 26 gcagaaagcgtctagccatgcgcgt 49

RESULT 20
AA085920
ID AA085920 standard; DNA; 37 BP.
XX
XX AA085920;
AC
XX
XX 02-NOV-1995 (first entry)
DE
XX Hepatitis C virus genome internal PCR primer YK-1030.
XX
XX Hepatitis C virus; HCV; non-A non-B; external PCR primer;
XX YK-1030; primer specific detection; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_feature 1..13
XX /tag= a
XX /note= "Oligo (du) sequence"
XX
XX WO9506753-A.
XX
XX 09-MAR-1995.
XX
XX 02-SEP-1994; 94WO-US09869.
```

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XX 03-SEP-1993: 93US-0116344.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Fields HA, Khudyakov YE;
XX WPI: 1995-115465/15.
XX
XX New method and kit for primer-specific detection of nucleic acids
XX - using two primers having a known sequence and a marker, resp
XX for solid-phase detection of amplification prods.
XX
XX Example 1: Page 12: 20pp: English.
XX
XX AA085918/19 are external, and AA085820/21 are internal PCR primers for
XX the Hepatitis C virus (HCV) genome. They were used to demonstrate
XX a new method for the primer specific detection of nucleic acids.
XX
XX Sequence 37 BP: 6 A; 6 C; 7 G; 5 T; 0 other;
SQ

```

Query Match 95.8%; Score 23; DB 16; Length 37;
 Best Local Similarity 100.0%; Pred. No. 0.00027;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 2 cagaagcgctcagccatgcgcgt 24
   |||||||||||||||||||
DB 14 cagaagcgctcagccatgcgcgt 36

```

RESULT 21
 ID AA075035 standard; DNA; 37 BP.
 AC AA075035;
 DT 04-AUG-1995 (first entry)
 DE PCR primer for the amplification of a peptide-streptavidin-oligo.
 XX Synthetic peptide: solid phase immunoassay; ss.
 OS Synthetic.
 PN WO9426932-A.
 PD 24-NOV-1994.
 PF 13-MAY-1994: 94WO-US05407.
 PR 13-MAY-1993: 93US-0061694.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Fields HA, Khudyakov YE;
 PI Fields HA, Khudyakov YE;
 DR WPI: 1995-006819/01.
 XX Solid phase immunoassay using oligo:nucleotide as label - also
 PT new conjugates of oligo:nucleotide coupled to antigenic peptide,
 PT partic. for diagnosing hepatitis C or E virus infection
 XX
 XX Example: Page 19: 34pp: English.
 XX
 XX AA082941 and AA082942 are examples of synthetic immunoreactive peptides.
 CC They are used in a method for detecting an antigen in a subject. The
 CC method involves binding the antigen to a solid support and then
 CC reacting it with an immunoreactive ligand (L) bound to an oligo;
 CC removing any unreacted L, and then detecting the presence of the
 CC oligo. A similar method can be used to detect Abs, in which case the
 CC ligand is an oligo-labelled Ag. The use of an amplifiable oligo as
 CC the label allows Ag or Ab to be detected at very low levels. In the

```

CC example, anti-human antibodies are adsorbed on the surface of
CC microcentrifuge tubes and used to capture antibodies from human
CC sera specimens. Then the tubes are incubated with a peptide-
CC streptavidin-oligo complex. After washing, PCR is performed, using
CC primers AA075034 and AA075035. AA075034 could be labelled with
CC another moiety, for example, biotin.
XX
XX Sequence 37 BP: 6 A; 6 C; 7 G; 5 T; 13 U; 0 other;
SQ

```

Query Match 95.8%; Score 23; DB 16; Length 37;
 Best Local Similarity 100.0%; Pred. No. 0.00027;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 2 cagaagcgctcagccatgcgcgt 24
   |||||||||||||||||||
DB 14 cagaagcgctcagccatgcgcgt 36

```

RESULT 22
 ID AA075033 standard; DNA; 58 BP.
 AC AA075033;
 DT 04-AUG-1995 (first entry)
 DE Biotinylated oligonucleotide.
 XX Synthetic peptide: solid phase immunoassay; ss.
 OS Synthetic.
 PN WO9426932-A.
 PD 24-NOV-1994.
 PF 13-MAY-1994: 94WO-US05407.
 PR 13-MAY-1993: 93US-0061694.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Fields HA, Khudyakov YE;
 PI Fields HA, Khudyakov YE;
 DR WPI: 1995-006819/01.
 XX Solid phase immunoassay using oligo:nucleotide as label - also
 PT new conjugates of oligo:nucleotide coupled to antigenic peptide,
 PT partic. for diagnosing hepatitis C or E virus infection
 XX
 XX Example: Page 18: 34pp: English.
 XX
 XX AA082941 and AA082942 are examples of synthetic immunoreactive peptides.
 CC They are used in a method for detecting an antigen in a subject. The
 CC method involves binding the antigen to a solid support and then
 CC reacting it with an immunoreactive ligand (L) bound to an oligo;
 CC removing any unreacted L, and then detecting the presence of the
 CC oligo. A similar method can be used to detect Abs, in which case the
 CC ligand is an oligo-labelled Ag. The use of an amplifiable oligo as
 CC the label allows Ag or Ab to be detected at very low levels. In the
 CC example, a synthetic peptide from the NS4 protein of the hepatitis
 CC C virus with structure (AA082943) is biotinylated using a
 CC commercially available kit. A biotinylated oligo with the structure
 CC 5'-biotinylated-AA075033-3' was prep'd. This oligo is composed
 CC of sequences of two PCR primers sepd. by a short additional
 CC sequence. The shorter the region to be amplified the better the
 CC efficiency of amplification obt'd. The biotinylated oligo is pre-

incubated with streptavidin. Then this complex linked by biotin-streptavidin binding. This INMA complex is then used in place of chemically prep. oligo-peptide conjugates mentioned above.

Sequence 58 BP; 10 A; 11 C; 15 G; 22 T; 0 other;

Query Match 95.8%; Score 23; DB 16; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 cagaagcgtctagcgcgt 24
|||||
Db 11 cagaagcgtctagcgcgt 33

RESULT 23

AA052817
ID AA052817 standard; RNA; 21 BP.

AC AA052817;

DT 26-MAY-1994 (first entry)

DE HCV target sequence 2.

RNA; enzyme; enzymatic RNA molecule; ERM; cleave; RNA; mRNA; HbRNA; plasmid; HIV; immunodeficiency virus; hepatitis B virus; HBV; papilloma virus; HPV; Epstein-Barr virus; EBV; T-cell leukemia virus; hepatitis C virus; HCV; cytomegalovirus; influenza virus; HSV; herpes simplex virus; vector; immune response; antibody; ribozyme; viral RNA; treatment; ss.

OS Synthetic.

PN WO9323569-A.

PD 25-NOV-1993.

PF 29-APR-1993; 93WO-US04020.

PR 11-MAY-1992; 92US-0882689.
PR 14-MAY-1992; 92US-0882712.
PR 14-MAY-1992; 92US-0882713.
PR 14-MAY-1992; 92US-0882714.
PR 14-MAY-1992; 92US-0882823.
PR 14-MAY-1992; 92US-0882824.
PR 14-MAY-1992; 92US-0882886.
PR 14-MAY-1992; 92US-0882888.
PR 14-MAY-1992; 92US-0882889.
PR 14-MAY-1992; 92US-0882921.
PR 14-MAY-1992; 92US-0883823.
PR 14-MAY-1992; 92US-0883849.
PR 14-MAY-1992; 92US-0884073.
PR 14-MAY-1992; 92US-0884074.
PR 14-MAY-1992; 92US-0884333.
PR 14-MAY-1992; 92US-0884422.
PR 14-MAY-1992; 92US-0884431.
PR 14-MAY-1992; 92US-0884436.
PR 14-MAY-1992; 92US-0884521.
PR 31-JUL-1992; 92US-0923738.
PR 26-AUG-1992; 92US-0936086.
PR 18-SEP-1992; 92US-0948359.
PR 15-OCT-1992; 92US-0963322.
PR 07-DEC-1992; 92US-0987129.
PR 07-DEC-1992; 92US-0987130.
PR 07-DEC-1992; 92US-0987133.

(RIBO-) RIBOZYME PHARM INC.

Draper KG, Dudycz LW, Holeczek JT, Macejak DG, Mamline JA;
McsWigen JA;

DR WPI; 1993-386599/48.

Enzymatic RNA molecules - used to inhibit viral replication,
infection and gene expression

Claim 5; Fig 12; 287pp; English.

The sequences (AA052816-052823) are pref. hepatitis C virus target sequences for enzymatic RNA molecules. The RNA molecules are complementary to a substrate binding region in the specified gene target. They also have enzymatic activity, in that they specifically cleave RNA in the target. The ERMs interfere with viral replication and therefore have anti-viral properties. They can be used to attenuate viruses to be used in vaccines.

Sequence 21 BP; 6 A; 5 C; 7 G; 3 U; 0 other;

Query Match 87.5%; Score 21; DB 14; Length 21;
Best Local Similarity 85.7%; Pred. No. 0.004;
Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaagcgtctagcgcgt 21
|||||
Db 1 gcagaagcgtctagcgcgt 21

RESULT 24

AAV70448
ID AAV70448 standard; DNA; 21 BP.

AC AAV70448;

DT 08-APR-1999 (first entry)

DE HCV target DNA amplifying 3' primer.

Nucleic acid detection; nucleic acid characterisation; hybridisation; infection; disease; cancer; forensic; paternity; multiplexing; HCV; PCR primer; ss.

Synthetic.
Hepatitis C virus.

PN WO9850403-A1.

PD 12-NOV-1998.

PF 05-MAY-1998; 98WO-US03194.

PR 03-MAR-1998; 98US-0034205.
PR 05-MAY-1997; 97US-0851588.
PR 19-SEP-1997; 97US-0934097.

(THIR-) THIRD WAVE TECHNOLOGIES INC.

Anderson TA, Brow MAD, Dahlberg JE, Dong F, Fors L;
Lyanichev VI, Neri BP, Prudent JR;
WPI; 1998-610317/51.

Detection and characterisation of nucleic acid sequences - by mixing a folded target and one or more probes to form a probe/folded target complex and detecting and characterising the complexes

Example 3; Page 116; 279pp; English.

The invention relates to methods and compositions of detection and characterisation of nucleic acid sequences and sequence changes. One method of detection and characterisation comprises: (a) providing: (1) a folded target having a DNA sequence comprising at least 1 double stranded region and at least 1 single stranded region; and (11) at least 1 probe complementary to at least a portion of the folded target; and

CC (b) mixing the target and probes so that the probe hybridises to form a
CC probe /folded target complex. Also provided are methods for determination
CC of structure formation in nucleic acid targets; for analysing folded
CC nucleic acids targets; and for analysis of nucleic acid structures. The
CC methods can be used for the detection and characterisation of nucleic
CC acid sequences to detect the presence of pathogenic nucleic acid
CC sequences indicative of an infection, the presence of variants or alleles
CC of mammalian genes associated with disease and cancers, and the
CC identification of the source of nucleic acids found in forensic samples,
CC as well as in paternity determinations. The methods allow simultaneous
CC analysis of both strands (e.g. the sense and antisense strands) and are
CC ideal for high-level multiplexing. The products produced are amenable to
CC qualitative, quantitative and positional analysis. The methods may be
CC performed in solution or in the solid phase (e.g. on a solid support).
CC The methods are powerful in that they allow for analysis of longer
CC fragments of nucleic acid than current methodologies. Sequences
CC AAV70447-48 represent primers used for the PCR amplification of hepatitis
CC C virus (HCV) target DNA used in the hybridisation analysis using
CC multiple capture probes for HCV genotyping.
CC
SQ Sequence 21 BP; 6 A; 5 C; 7 G; 3 T; 0 other;

Query Match 87.5%; Score 21; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaagcgtctagcattg 21
|||||
Db 1 gcagaagcgtctagcattg 21

RESULT 25
AAAT2990/C
ID AAA72990 standard; DNA; 21 BP.
XX
AC AAA72990;
XX
DT 24-NOV-2000 (first entry)
XX
DE Hepatitis C virus antisense oligonucleotide HCV88.
XX
KW Hepatitis C virus; HCV; antisense oligonucleotide; leuciferinase;
KW luciferase; HepG2; medicine; ss.
XX
OS Hepatitis C virus.
XX
PN CN1253138-A.
XX
PD 17-MAY-2000.
XX
PF 09-NOV-1998; 98CN-0124388.
XX
PR 09-NOV-1998; 98CN-0124388.
XX
PA (RADT-) RADIMEDICINE ACAD MILITARY MEDICAL SCI.
XX
PI Wang S, Wang X, Zhu B;
XX
DR WPI: 2000-466526/41.
XX
PT Structure and usage of antisense oligonucleotide for treating diseases
PT correlative to hepatitis C virus -
XX
PS Claim 1; Page 1; 20pp; Chinese.
XX
CC The present invention describes antisense oligonucleotides which are
CC designed and synthesised on the basis of the gene structure of
CC hepatitis C virus (HCV) and can be used to suppress the expression of
CC HCV gene. The non-coding region 5' of HCV gene is used to regulate the
CC instantaneous expression system of leuciferinase gene in HepG2 cells
CC and the transgenic cell model HepG2.9706 of luciferase gene. The 15
CC antisense oligonucleotides (AAAT2988 to AAAT3002) which are complementary

CC to the non-coding region 5' and translational initiation region of HCV
CC are actively screened and evaluated to discover for the first time the
CC oligonucleotides HCV279, HCV349, HCV363, HCV65 and HCV 313 and their
CC chemical modified objects for suppressing the expression of HCV gene.
CC Thus, the present invention relates to the new medicine for treating the
CC diseases associated with HCV.
CC
SQ Sequence 21 BP; 3 A; 7 C; 5 G; 6 T; 0 other;

Query Match 87.5%; Score 21; DB 21; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaagcgtctagcattg 21
|||||
Db 21 GCAGAAAGCGTCTAGCCATCG 1

RESULT 26
AAH79078
ID AAH79078 standard; DNA; 21 BP.
XX
AC AAH79078;
XX
DT 20-NOV-2001 (first entry)
XX
DE HCV negative strand RNA sense PCR primer.
XX
KW Transgenic animal model; human hepatotropic pathogen; immunotherapy;
KW human hepatitis C virus; HCV; vaccine; antiviral; hyperlipidaemia;
KW atherosclerosis; PCR primer; ss.
XX
OS Hepatitis C virus.
OS Synthetic.
XX
PN WO200167854-A1.
XX
PD 20-SEP-2001.
XX
PF 16-MAR-2001; 2001WO-CA00350.
XX
PR 17-MAR-2000; 2000US-0528120.
XX
PA (KNET/) KNETEMAN N M.
PA (TYRR/) TYRRELL D L.
PA (MERC/) MERCER D F.
XX
PI Kneteman NM, Tyrrell DL, Mercer DF;
XX
DR WPI: 2001-582368/65.
XX
PT New chimeric immunodeficient transgenic murine host susceptible to
PT hepatitis C virus infection, useful as model for screening compounds,
PT comprises chimeric liver, where transgene encodes urokinase-type
PT plasmidogen activator -
XX
PS Example 4; Page 38; 78pp; English.
XX
CC The invention relates to a non-human animal model that is susceptible to
CC infection by human hepatotropic pathogens, especially human hepatitis C
CC virus (HCV). The model is based on a non-human, immunocompromised
CC xenogeneic transgenic animal having a human-mouse chimeric liver. The
CC invention outlines the creation of a chimeric immunodeficient murine host
CC infected with human HCV and deficient in functional syngeneic B and T
CC lymphocytes, comprising a genomically integrated transgene encoding a
CC urokinase-type plasminogen activator in liver cells and a chimeric liver
CC comprising human hepatocytes engrafted into liver of the murine host,
CC where inoculation of chimeric host with HCV results in HCV infection. The
CC chimeric mouse model is useful for culturing human HCV, for screening
CC candidate agents for activity against a hepatotropic pathogen,
CC especially a vaccine for active immunotherapy or for therapeutic
CC vaccination or an immunotherapeutic agent e.g. anti-HCV body or

CC HCV-binding fragment, for evaluating liver toxicity of an agent, for the
CC development of antiviral agents and also as animal model for
CC hyperlipidaemic and atherosclerosis. The animal model provides the first
CC instance of an animal that is susceptible to infection by HCV through the
CC normal route of infection and further it can become more chronically,
CC consistently and stably infected at viral titers that can be equated to
CC viral titers in HCV-infected humans. The present sequence is that of a
CC PCR primer for detection of negative-stranded HCV RNA.
XX
SQ Sequence 21 BP; 5 A; 5 C; 7 G; 4 T; 0 other;

Query Match 87.5%; Score 21; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 gaagcgtctagccatgcgtc 24
|||||
Db 1 gaagcgtctagccatgcgtc 21

RESULT 27

ABA01127
ID ABA01127 standard; DNA; 21 BP.

AC ABA01127;

DT 06-FEB-2002 (first entry)

DE HCV primer Outer F.

XX Hepatitis C virus; HCV; nucleic acid synthesis;

KM complementary chain synthesis; diagnosis; primer; ss.

XX Hepatitis C virus.

OS WO200177317-A1.

PN 18-OCT-2001.

XX 30-MAR-2001; 2001WO-JP02771.

PF 07-APR-2000; 2000JP-0111939.

PR (EIKE) EIKEN KAGAKU KK.

PA Notomi T, Nagamine K;

XX WPI; 2002-010907/01.

DR Isothermal amplification of nucleic acids using double-stranded nucleic
XX acid as template to establish complementary chain synthesis reaction
PT from primer enabling base pairing in domain to be annealed, useful e.g.
PT in gene diagnosis -

PS Example 1; Page 41; 75pp; Japanese.

XX The invention relates to a method for synthesising a nucleic acid using
CC a double-stranded nucleic acid as template and incubating under
CC conditions allowing the establishment of a complementary chain synthesis
CC reaction. The method uses an arbitrary primer to initiate the
CC complementary chain synthesis reaction. The method is particularly
CC useful in gene and disease diagnosis. It is a highly efficient and
CC reaction specific method in which no temperature variation is required.
CC The present sequence is a primer used in an example illustrating the
CC invention.
XX

SQ Sequence 21 BP; 6 A; 5 C; 7 G; 3 T; 0 other;

Query Match 87.5%; Score 21; DB 24; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gcagaagcgtctagccatgc 21
|||||
Db 1 gcagaagcgtctagccatgc 21

RESULT 28

AAH79081
ID AAH79081 standard; DNA; 24 BP.

AC AAH79081;

DT 20-NOV-2001 (first entry)

DE HCV PCR primer SEQ ID NO 5.

XX Transgenic animal model; human hepatotropic pathogen; immunotherapy;
KM human hepatitis C virus; HCV; vaccine; antiviral; hyperlipidaemia;
KM atherosclerosis; PCR primer; ss.

OS Hepatitis C virus.
XX Synthetic.

PN WO200167854-A1.

PD 20-SEP-2001.

PF 16-MAR-2001; 2001WO-CA00350.

PR 17-MAR-2000; 2000US-0528120.

XX (KNET/) KNETEMAN N M.

PA (TYRR/) TYRRELL D L.

XX (MERC/) MERCER D F.

PI Kneteman NM, Tyrrell DL, Mercer DF;

DR WPI; 2001-582368/65.

XX New chimeric immunodeficient transgenic murine host susceptible to
PT hepatitis C virus infection, useful as model for screening compounds,
PT comprises chimeric liver, where transgene encodes urokinase-type
PT plasminogen activator -

PS Example 4; Page 39; 78pp; English.

XX The invention relates to a non-human animal model that is susceptible to
CC infection by human hepatotropic pathogens, especially human hepatitis C
CC virus (HCV). The model is based on a non-human, immunocompromised
CC xenogeneic transgenic animal having a human-mouse chimeric liver. The
CC invention outlines the creation of a chimeric immunodeficient murine host
CC infected with human HCV and deficient in functional syngeneic B and T
CC lymphocytes, comprising a genomically integrated transgene encoding a
CC urokinase-type plasminogen activator in liver cells and a chimeric liver
CC comprising human hepatocytes engrafted into liver of the murine host,
CC where inoculation of chimeric host with HCV results in HCV infection. The
CC chimeric mouse model is useful for culturing human HCV, for screening
CC candidate agents for actively against a hepatotropic pathogen,
CC especially a vaccine for active immunotherapy or for therapeutic
CC vaccination or an immunotherapeutic agent e.g. anti-HCV body or
CC HCV-binding fragment, for evaluating liver toxicity of an agent, for the
CC development of antiviral agents and also as animal model for
CC hyperlipidaemic and atherosclerosis. The animal model provides the first
CC instance of an animal that is susceptible to infection by HCV through the
CC normal route of infection and further it can become more chronically,
CC consistently and stably infected at viral titers that can be equated to
CC viral titers in HCV-infected humans. The present sequence is that of a
CC PCR primer useful in a method for detection of negative-stranded HCV RNA
CC by RNase protection assay.
XX

SQ Sequence 24 BP; 6 A; 5 C; 8 G; 5 T; 0 other;

Query Match 87.5%; Score 21; DB 22; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.004;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 gaaagcgtctagccatgagcgt 24
 |||
 Db 1 gaaagcgtctagccatgagcgt 21

RESULT 29

AA098291
 ID AA098291 standard; DNA; 25 BP.

XX AA098291;

DT 19-MAR-1996 (first entry)

DE Hepatitis C virus sense PCR detection primer P21.

KW Primer; hepatitis C virus; PCR; amplification; reverse transcription;
 detection; non-translated region; ss.

XX OS Synthetic.

PN JP07184695-A.

PD 25-JUL-1995.

PF 27-DEC-1993; 93JP-0332682.

PR 27-DEC-1993; 93JP-0332682.

PA (SANWA) SANWA KAGAKU KENKYUSHO CO LTD.

DR WPI; 1995-287992/38.

PT Simple detection of Hepatitis C virus in a single reaction tube -
 useful for high sensitivity and ease of reproduction.

XX Example 3; Page 7; 14pp; Japanese.

CC The primers AA098270-94 are used in a novel simple method for the
 detection of hepatitis C virus. The novel method involves the steps of
 extracting the virus from a sample, synthesizing cDNA from the viral RNA
 by reverse transcription, amplifying the cDNA by a first PCR and
 reamplifying the amplified product in a second PCR, all of which occur in
 a single reaction tube. The primers are designed based on a 334 bp
 sequence (AA098272) derived from a 5' non-translated region of the viral
 genome. This primer corresponds to bases 54-78 of AA098272.

XX SQ Sequence 25 BP; 6 A; 5 C; 8 G; 6 T; 0 other;

Query Match 87.5%; Score 21; DB 16; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.004;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 gaaagcgtctagccatgagcgt 24
 |||
 Db 1 gaaagcgtctagccatgagcgt 21

Search completed: August 26, 2002, 22:24:55
 Job time: 6234 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 19:12:26 ; Search time 1915.63 Seconds
(without alignments)
262.178 Million cell updates/sec

Title: US-10-037-990A-1

Perfect score: 24
Sequence: 1 gcagaagcgtctagccatg9cgt 24

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size: 21

Total number of hits satisfying chosen parameters: 25

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database:

GenEmbl:*
1: gb_da:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
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17: em_hum:*
18: em_in:*
19: em_inu:*
20: em_om:*
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22: em_ov:*
23: em_pat:*
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25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlgo_inv:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Match Length	ID	Description
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1	24	100.0	24	6	A68287	A68287 Sequence 8
2	24	100.0	24	6	AR054578	AR054578 Sequence
3	24	100.0	24	6	AX003941	AX003941 Sequence
4	24	100.0	24	6	AX021563	AX021563 Sequence
5	24	100.0	24	6	AX021622	AX021622 Sequence
6	24	100.0	24	6	AX147011	AX147011 Sequence
7	24	100.0	24	6	AX250664	AX250664 Sequence
8	24	100.0	24	6	I22146	I22146 Sequence 5
9	24	100.0	24	6	I26949	I26949 Sequence 17
10	24	100.0	24	6	I40301	I40301 Sequence 9
11	24	100.0	24	6	I59678	I59678 Sequence 9
12	24	100.0	24	6	I68634	I68634 Sequence 7
13	24	100.0	24	6	AR054575	AR054575 Sequence
14	24	100.0	24	6	AR094137	AR094137 Sequence
15	24	100.0	24	6	AX147021	AX147021 Sequence
16	24	100.0	24	6	I22147	I22147 Sequence 6
17	24	100.0	24	6	AX021612	AX021612 Sequence
18	24	100.0	24	6	AX172761	AX172761 Sequence
19	23	95.8	28	6	BD000263	BD000263 Oligonuc
20	21	87.5	21	6	AR131532	AR131532 Sequence
21	21	87.5	21	6	AR144109	AR144109 Sequence
22	21	87.5	21	6	AX250669	AX250669 Sequence
23	21	87.5	21	6	BD001049	BD001049 Method an
24	21	87.5	21	6	BD001478	BD001478 Method an
25	21	87.5	24	6	AX250672	AX250672 Sequence

ALIGNMENTS

RESULT	1	A68287	24 bp	DNA	linear	PAT 06-MAY-1999
LOCUS	A68287	Sequence 8 from Patent WO9746716.				
DEFINITION	A68287					
ACCESSION	A68287	GI:4759408				
VERSION	A68287.1					
KEYWORDS						
SOURCE		unidentified.				
ORGANISM		unidentified.				
REFERENCE	1 (bases 1 to 24)					
AUTHORS	Bosio, P., Strumila, C. and Clemenza, F.					
METHOD	TO DETECT HCV SPECIFIC NUCLEIC ACIDS					
TITLE	Patent: WO 9746716-A 8 11-DEC-1997;					
JOURNAL	WABCO B V (NL)					
COMMENT	Other publication IT RM960404 19971209.					
FEATURES	Location/Qualifiers					
source	1..24					
BASE COUNT	6 a 6 c 8 g 4 t					
ORIGIN						

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcagaagcgtctagccatg9cgt 24
Db 1 GCAGAAAGCGCTTAGCCATGCGT 24

RESULT	2	AR054578	24 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR054578	Sequence 4 from patent US 5837442.				
DEFINITION	AR054578					
ACCESSION	AR054578	GI:5980155				
VERSION	AR054578.1					
KEYWORDS						
SOURCE		Unknown.				
ORGANISM		Unknown.				
		Unclassified.				

REFERENCE 1 (bases 1 to 24)
AUTHORS Tsang,S.Yen.
TITLE Oligonucleotide primers for amplifying HCV nucleic acid
JOURNAL Patent: US 5837442-A 4 17-NOV-1998;
FEATURES Location/Qualifiers
SOURCE 1..24
/organism="unknown"
BASE COUNT 6 a 6 c 8 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaaagcgtctagccatgacgt 24
|||||
Db 1 GCAGAAAGCGTCTAGCCATGCGCT 24

RESULT 3
AX003941 24 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 1 from Patent WO9923249.
ACCESSION AX003941
VERSION AX003941.1 GI:9927601
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 24)
AUTHORS Kessler,C., Bartl,K., Habermussen,G. and Orum,H.
TITLE Specific and sensitive method for detecting nucleic acids
JOURNAL Patent: WO 9923249-A 1 14-MAY-1999;
KESSLER CHRISTOPH (DE); BARTL KNUDT (DE); HABERHAUSEN GERD (DE);
ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES Location/Qualifiers
SOURCE 1..24
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Ky80"

BASE COUNT 6 a 6 c 8 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaaagcgtctagccatgacgt 24
|||||
Db 1 GCAGAAAGCGTCTAGCCATGCGCT 24

RESULT 4
AX021563 24 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 1 from Patent WO9924606.
ACCESSION AX021563
VERSION AX021563.1 GI:10044847
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 24)
AUTHORS Kessler,C., Bartl,K., Habermussen,G. and Orum,H.
TITLE Specific and sensitive nucleic acid detection method
JOURNAL Patent: WO 9924606-A 1 20-MAY-1999;
KESSLER CHRISTOPH (DE); BARTL KNUDT (DE); HABERHAUSEN GERD (DE);
ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES Location/Qualifiers
SOURCE 1..24

BASE COUNT 6 a 6 c 8 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaaagcgtctagccatgacgt 24
|||||
Db 1 GCAGAAAGCGTCTAGCCATGCGCT 24

RESULT 5
AX021622 24 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 1 from Patent WO9923250.
ACCESSION AX021622
VERSION AX021622.1 GI:10044905
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 24)
AUTHORS Kessler,C., Bartl,K., Habermussen,G. and Orum,H.
TITLE Specific and sensitive method for detecting nucleic acids
JOURNAL Patent: WO 9923250-A 1 14-MAY-1999;
KESSLER CHRISTOPH (DE); BARTL KNUDT (DE); HABERHAUSEN GERD (DE);
ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES Location/Qualifiers
SOURCE 1..24
/organism="Hepatitis C virus"
/db_xref="taxon:11103"

BASE COUNT 6 a 6 c 8 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaaagcgtctagccatgacgt 24
|||||
Db 1 GCAGAAAGCGTCTAGCCATGCGCT 24

RESULT 6
AX147011 24 bp DNA linear PAT 08-JUN-2001
LOCUS
DEFINITION Sequence 5 from Patent WO0137291.
ACCESSION AX147011
VERSION AX147011.1 GI:14346282
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 24)
AUTHORS Weindel,K., Riedling,M. and Geiger,A.
TITLE Magnetic glass particles, method for their preparation and uses thereof
JOURNAL Patent: WO 0137291-A 5 25-MAY-2001;
Roche Diagnostics GmbH (DE)
FEATURES Location/Qualifiers
SOURCE 1..24
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide primer (HCV forward)"

BASE COUNT 6 a 6 c 8 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcagaaagcgtctagccatgagcgt 24
DB 1 GCAGAAAGCGTCTAGCCATGAGCGGT 24

RESULT 7
LOCUS AX250664 24 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 60 from Patent WO0168921.
ACCESSION AX250664
VERSION AX250664.1 GI:15984408
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 24)
AUTHORS Koshinsky H., Zwick M.S. and McCue K.F.
TITLE Compositions and methods for simultaneous detection of multiple biological entities
JOURNAL Patent: WO 0168921-A 60 20-SEP-2001;
Investigen (US)
FEATURES Location/Qualifiers
source 1..24
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR Primer"
BASE COUNT 6 a 6 c 8 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcagaaagcgtctagccatgagcgt 24
DB 1 GCAGAAAGCGTCTAGCCATGAGCGGT 24

RESULT 8
LOCUS I22146 24 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 5 from patent US 5527669.
ACCESSION I22146
VERSION I22146.1 GI:1602500
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Resnick, R.M. and Young, K.K.Y.
TITLE Methods, primers and probes for detection of hepatitis C and novel variants
JOURNAL Patent: US 5527669-A 5 18-JUN-1996;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
BASE COUNT 6 a 6 c 8 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcagaaagcgtctagccatgagcgt 24
DB 1 GCAGAAAGCGTCTAGCCATGAGCGGT 24

RESULT 9
LOCUS I26949 24 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 17 from patent US 5561038.
ACCESSION I26949
VERSION I26949.1 GI:1606819
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gelfand, D.H., Myers, T.W. and Signa, C.L.
TITLE Methods for coupled high temperatures reverse transcription and polymerase chain reactions
JOURNAL Patent: US 5561038-A 17 01-OCT-1996;
FEATURES Location/Qualifiers
source 1..24
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BASE COUNT 6 a 6 c 8 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcagaaagcgtctagccatgagcgt 24
DB 1 GCAGAAAGCGTCTAGCCATGAGCGGT 24

RESULT 10
LOCUS I40301 24 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 9 from patent US 5620852.
ACCESSION I40301
VERSION I40301.1 GI:2082593
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Lin, L., Cimino, G. and Zhu, Y.S.
TITLE Nucleic acid preparation methods
JOURNAL Patent: US 5620852-A 9 15-APR-1997;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
BASE COUNT 6 a 6 c 8 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcagaaagcgtctagccatgagcgt 24
DB 1 GCAGAAAGCGTCTAGCCATGAGCGGT 24

RESULT 11
LOCUS I59678 24 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 9 from patent US 5654179.
ACCESSION I59678
VERSION I59678.1 GI:2478310
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Resnick, R.M. and Young, K.K.Y.
TITLE Methods, primers and probes for detection of hepatitis C and novel variants
JOURNAL Patent: US 5527669-A 5 18-JUN-1996;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
BASE COUNT 6 a 6 c 8 g 4 t
ORIGIN

REFERENCE 1 (bases 1 to 24)
AUTHORS Lin, L.
TITLE Nucleic acid preparation methods
JOURNAL Patent: US 5654179-A 9 05-AUG-1997;
FEATURES Location/Qualifiers
source 1..24

BASE COUNT 6 a 6 c 8 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaaagcgtctagccatggcgt 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 12
168634
LOCUS 168634
DEFINITION Sequence 7 from patent US 5677124.
ACCESSION 168634
VERSION 168634.1 GI:2830756
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dubois, D.B., Winkler, M.M. and Pasloske, B.L.
TITLE Ribonuclease resistant viral RNA standards
JOURNAL Patent: US 5677124-A 7 14-OCT-1997;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"

BASE COUNT 6 a 6 c 8 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaaagcgtctagccatggcgt 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 13
AR054575
LOCUS AR054575
DEFINITION Sequence 1 from patent US 5837442.
ACCESSION AR054575
VERSION AR054575.1 GI:5980152
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Tsang, S.Yen.
TITLE Oligonucleotide primers for amplifying HCV nucleic acid
JOURNAL Patent: US 5837442-A 1 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..26
/organism="unknown"

BASE COUNT 7 a 6 c 8 g 5 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0018;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaaagcgtctagccatggcgt 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 14
AR094137
LOCUS AR094137
DEFINITION Sequence 3 from patent US 6001611.
ACCESSION AR094137
VERSION AR094137.1 GI:10020882
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Will, S.Gordon.
TITLE Modified nucleic acid amplification primers
JOURNAL Patent: US 6001611-A 3 14-DEC-1999;
FEATURES Location/Qualifiers
source 1..26
/organism="unknown"

BASE COUNT 7 a 6 c 8 g 5 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaaagcgtctagccatggcgt 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 15
AX147021
LOCUS AX147021
DEFINITION Sequence 15 from Patent WO0137291.
ACCESSION AX147021
VERSION AX147021.1 GI:14346292
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 26)
AUTHORS Weinidel, K., Riedling, M. and Geiger, A.
TITLE Magnetic glass particles, method for their preparation and uses thereof
JOURNAL Patent: WO 0137291-A 15 25-MAY-2001;
FEATURES Roche Diagnostics GmbH (DE)
source Location/Qualifiers
1..26
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide primer (HCV forward)"
/note="derivatization with a p-(t-butyl)benzyl-residue"
modified_base 26
/mod_base=OTHER

BASE COUNT 7 a 6 c 8 g 5 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaaagcgtctagccatggcgt 24
Db 1 GCAGAAAGCGTCTAGCCATGGCGT 24

RESULT 16
LOCUS 122147 26 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 6 from patent US 5527669.
ACCESSION 122147
VERSION 122147.1 GI:1602501
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Resnick,R.M. and Young,K.K.Y.
TITLE Methods, primers and probes for detection of hepatitis C and novel variants
JOURNAL Patent: US 5527669-A 6 18-JUN-1996;
FEATURES
source Location/Qualifiers
BASE COUNT 7 a 7 c 8 g 4 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaagcgtctagccatgagcgt 24
|||||
DB 3 GCAGAAAGCGCTAGCCATGCGCT 26

RESULT 17
LOCUS AX021612 51 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 50 from Patent WO9924606.
ACCESSION AX021612
VERSION AX021612.1 GI:10044896
KEYWORDS
SOURCE Hepatitis C virus.
ORGANISM Hepatitis C virus.
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepcivirus.
REFERENCE 1 (bases 1 to 51)
AUTHORS Kessler,C., Bartl,K., Habershausen,G. and Orum,H.
TITLE Specific and sensitive nucleic acid detection method
JOURNAL Patent: WO 9924606-A 50 20-MAY-1999;
KESLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE); ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES
source Location/Qualifiers
1. 51
/organism="Hepatitis C virus"
/db_xref="taxon:11103"
BASE COUNT 11 a 12 c 15 g 13 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaagcgtctagccatgagcgt 24
|||||
DB 8 GCAGAAAGCGCTAGCCATGCGCT 31

RESULT 18
LOCUS AX172761 77 bp mRNA linear PAT 03-JUL-2001
DEFINITION Sequence 9 from Patent WO0144266.
ACCESSION AX172761
VERSION AX172761.1 GI:14597857
KEYWORDS

SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 77)
AUTHORS Karn,J.C. and Walker,S.C.
TITLE Nucleic acid compounds and screening assays using the same
JOURNAL Patent: WO 0144266-A 9 21-JUN-2001;
RiboTargets Limited (GB)
FEATURES
source Location/Qualifiers
1. 77
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Probe"
BASE COUNT 16 a 20 c 23 g 18 t
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gcagaagcgtctagccatgagcgt 24
|||||
DB 26 GCAGAAAGCGCTAGCCATGCGCT 49

RESULT 19
LOCUS BD000263 28 bp DNA linear PAT 31-JAN-2002
DEFINITION Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof.
ACCESSION BD000263
VERSION BD000263.1 GI:18623342
KEYWORDS JP 2000279200-A/1.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 28)
AUTHORS Lynen,J.M. and Gorman,K.M.
TITLE Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof
JOURNAL Patent: JP 2000279200-A 1 10-OCT-2000;
ORTHO CLINICAL DIAGNOSTICS INC
COMMENT
OS Artificial Sequence
PN JP 2000279200-A/1
PD 10-OCT-2000
PF 03-FEB-2000 JP 2000032656
PR 03-FEB-1999 US 60/118497
PI JEFFREY M LYNNEN,KEVIN M GORMAN
PC C12Q1/68,C12N15/09/(C12N15/09,C12R1:92),C12N15/00,(C12N15/00,C12R1:92)
CC
FH
FT Key
FT source Location/Qualifiers
1. 28
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 8 a 6 c 8 g 6 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.0069;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 cagaagcgtctagccatgagcgt 24
|||||
DB 1 CAGAAAGCGCTAGCCATGCGCT 23

RESULT 20

AR131532
LOCUS AR131532 21 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 25 from patent US 6194149.
ACCESSION AR131532
VERSION AR131532.1 GI:14120435
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Nerl, B., Dong, F., Lyamichiev, V., Brow, M. And, and Fors, L.
TITLE Target-dependent reactions using structure-bridging oligonucleotides
JOURNAL Patent: US 6194149-A 25 27-FEB-2001;
FEATURES
source Location/Qualifiers
1..21
BASE COUNT 6 a 5 c 7 g 3 t
ORIGIN

Query Match 87.5%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gcagaaagcgtctagccatg 21
|||||
Db 1 GCAGAAAGCGCTAGCCATG 21

RESULT 21
LOCUS AR144109 21 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 25 from patent US 6210880.
ACCESSION AR144109
VERSION AR144109.1 GI:15105976
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Lyamichiev, V.I., Dong, F., Brow, M. And, Fors, L. and Nerl, B.P.
TITLE Polymorphism analysis by nucleic acid structure probing with structure-bridging oligonucleotides
JOURNAL Patent: US 6210880-A 25 03-APR-2001;
FEATURES
source Location/Qualifiers
1..21
BASE COUNT 6 a 5 c 7 g 3 t
ORIGIN

Query Match 87.5%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gcagaaagcgtctagccatg 21
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Db 1 GCAGAAAGCGCTAGCCATG 21

RESULT 22
LOCUS AX250669 21 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 2 from Patent W00167854.
ACCESSION AX250669
VERSION AX250669.1 GI:15984413
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 21)
AUTHORS Kneeteman, N.M., Tyrrell, L.D. and Mercer, D.F.

TITLE Chimeric animal model susceptible to human hepatitis c virus
JOURNAL Infection
Patent: WO 0167854-A 2 20-SEP-2001;
Kneeteman, Norman M. (CA) ; Tyrrell, Lorne D. (CA) ; Mercer, David F. (CA)
FEATURES
source Location/Qualifiers
1..21
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer"
BASE COUNT 5 a 5 c 7 g 4 t
ORIGIN

Query Match 87.5%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 gaaagcgtctagccatg 24
|||||
Db 1 GAAAGCGCTAGCCATGCGCT 21

RESULT 23
LOCUS BD001049 21 bp RNA linear PAT 31-JAN-2002
DEFINITION Method and reagent for inhibiting viral replication.
ACCESSION BD001049
VERSION BD001049.1 GI:18625608
KEYWORDS JP 2000342285-A/209.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 21)
AUTHORS Draper, K.G., Dadykiz, L.W., Macswigen, J.A., Maysejak, D.G.,
Holesek, J.J. and Mamone, A.J.
TITLE Method and reagent for inhibiting viral replication
JOURNAL Patent: JP 2000342285-A 209 12-DEC-2000;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2000342285-A/209
PD 12-DEC-2000
PF 01-MAY-2000 JP 2000132616
PR 11-MAY-1992 US 07/882689, 14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713, 14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823, 14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882866, 14-MAY-1992 US 07/882868 PR
14-MAY-1992 US 07/882889, 14-MAY-1992 US 07/882921 PR
14-MAY-1992 US 07/882922, 14-MAY-1992 US 07/883823 PR
14-MAY-1992 US 07/883849, 14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074, 14-MAY-1992 US 07/884333 PR
14-MAY-1992 US 07/884422, 14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436, 14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738, 26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086, 18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322, 07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130, 07-DEC-1992 US 07/987133 PI
KENNETH G DRAPER, LEC W DADYKIZ, JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLESEK, ANTHONY J MAMONE
PC C12N15/00,
C12N15/09, C12N5/10, C12N7/00, C12N9/22//((C12N5/10, C12R1:91), PC
C12N5/00, (C12N5/00, C12R1:91)
CC
FH key Location/Qualifiers
FT source 1..21
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1..21
Location/Qualifiers
1..21
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/db_xref="taxon:32630"
BASE COUNT 6 a 5 c 7 g 3 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcagaaagcgtacgcatg 21
|||||
DB 1 GCAGAAAGCGTACGCAATG 21

RESULT 24
BD001478 21 bp RNA linear PAT 31-JAN-2002
LOCUS BD001478 Method and reagent for inhibiting viral replication.
DEFINITION BD001478
ACCESSION BD001478.1 GI:18626037
VERSION JP 2000342286-A/209.
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 21)
AUTHORS Draper,K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
TITLE Holesek,J.J. and Mamone,A.J. Inhibiting viral replication
JOURNAL Patent: JP 2000342286-A 209 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2000342286-A/209
PD 12-DEC-2000
PR 01-MAY-2000 JP 2000132651
PR 11-MAY-1992 US 07/882689, 14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713, 14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823, 14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882866, 14-MAY-1992 US 07/882868 PR
14-MAY-1992 US 07/882869, 14-MAY-1992 US 07/882891 PR
14-MAY-1992 US 07/882922, 14-MAY-1992 US 07/883823 PR
14-MAY-1992 US 07/883849, 14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074, 14-MAY-1992 US 07/884333 PR
14-MAY-1992 US 07/884422, 14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436, 14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738, 26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086, 18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322, 07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130, 07-DEC-1992 US 07/987133 PI
KENNETH G DRAPER, LEC W DADYKTZ, JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLESER, ANTHONY J MAMONE
PC C12N15/09, C12N5/10, C12N7/00//A61K38/43, A61K39/125, A61K39/13,
PC A61K39/135,
PC A61K39/145, A61K39/21, A61K39/23, A61K39/245, A61K39/29, A61K48/00,
PC A61P1/16,
PC A61P31/14, A61P31/16, A61P31/18, A61P31/22, A61P35/02, C12O1/68, PC
(C12N15/09, C12N15/93), C12N15/00, C12N5/00, A61K37/48, (C12N15/00, PC
C12R1/93)
CC
FH Key Location/Qualifiers
FT source 1. 21
FT /organism="Artificial Sequence".
FEATURES
source 1. 21
Location/Qualifiers
BASE COUNT 6 a 5 c 7 g 3 t
ORIGIN

Query Match 87.5%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcagaaagcgtacgcatg 21
|||||
DB 1 GCAGAAAGCGTACGCAATG 21

DB 1 GCAGAAAGCGTACGCAATG 21

RESULT 25
AX250672 24 bp DNA linear PAT 05-OCT-2001
LOCUS AX250672 Sequence 5 from Patent WO0167854.
DEFINITION AX250672
ACCESSION AX250672
VERSION AX250672.1 GI:15984416
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 24)
AUTHORS Kneeteman,N.M., Tyrrell,L.D. and Mercer,D.F.
TITLE Chimeric animal model susceptible to human hepatitis c virus
JOURNAL Infection
Patent: WO 0167854-A 5 20-SEP-2001;
Kneeteman, Norman M. (CA) ; Tyrrell, Lorne D. (CA) ; Mercer, David
F. (CA)
FEATURES
source 1. 24
Location/Qualifiers
BASE COUNT 6 a 5 c 8 g 5 t
ORIGIN

Query Match 87.5%; Score 21; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 gaagcgtacgcatgacgt 24
|||||
DB 1 GAAGCGTACGCAATGCGCT 21

Search completed: August 26, 2002, 21:20:52
Job time: 7706 sec

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OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 19:44:36 ; Search time 3233.25 Seconds
(without alignments)
100.186 Million cell updates/sec

Title: US-10-037-990A-1

Perfect score: 24
Sequence: 1 gcagaaagcgtctagccatgycgt 24

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 21

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
No matches found					

Search completed: August 26, 2002, 22:14:58
Job time: 9022 sec

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OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 22:14:58 ; Search time 3233.25 Seconds
(without alignments)
87.663 Million cell updates/sec

Title: US-10-037-990A-3

Perfect score: 21
Sequence: 1 gtcgtgcagcctccagagacc 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 21

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database :

EST:*

1: em_estba:*\n2: em_esthum:*\n3: em_estlin:*\n4: em_estmu:*\n5: em_estrov:*\n6: em_estcpl:*\n7: em_esttro:*\n8: em_hlc:*\n9: gb_est1:*\n10: gb_est2:*\n11: gb_hlc:*\n12: gb_gss:*\n13: em_gss_hum:*\n14: em_gss_inv:*\n15: em_gss_pln:*\n16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description
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No matches found

Search completed: August 26, 2002, 22:14:58
Job time: 9022 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 22:17:12 ; Search time 119.4 Seconds
(without alignments)
43.202 Million cell updates/sec

Title: US-10-037-990A-3

Perfect score: 21

Sequence: 1 gtctgagcctccagacc 21

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 21

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database : Issued_Patents_NA:*

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- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query		
No.	Score	Match length	ID

Description			

No matches found

Search completed: August 26, 2002, 22:17:12
Job time: 5905 sec

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PR 03-FEB-1999 US 60/118497
PI JEFFREY M LYNE, KEVIN M GORMAN
PC C12Q1/68, C12N15/09//((C12N15/09, C12R1:92), C12N15/00, (C12N15/00,
PC C12R1:92))
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FT source 1. .27 Location/Qualifiers
/organism='Artificial Sequence',
location/Qualifiers
1. .27
/organism='synthetic construct',
/db_xref='taxon:32630'
BASE COUNT 5 a 8 c 9 g 5 t
ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtcgtcagcctccagacc 21
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Db 21 GTCGTCAAGCCTCCAGACC 1

RESULT 3
AX003946 48 bp DNA linear PAT 24-AUG-2000
LOCUS
DEFINITION Sequence 6 from Patent WO923249.
ACCESSION AX003946
VERSION AX003946.1 GI:9927606
KEYWORDS
SOURCE Hepatitis C virus.
ORGANISM Hepatitis C virus.
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepadnavirus.
REFERENCE 1 (bases 1 to 48)
AUTHORS Kessler, C., and Bartl, K.
TITLE Specific and sensitive method for detecting nucleic acids.
JOURNAL Patent: WO 9923249-A 6 14-MAY-1999;
KESSLER CHRISTOPH (DE); BARTL KNOT (DE)
FEATURES
source
1. .48
/organism='Hepatitis C virus',
/db_xref='taxon:11103'

BASE COUNT 9 a 18 c 14 g 7 t
ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtcgtcagcctccagacc 21
|||||
Db 10 GTCGTCAAGCCTCCAGACC 30

RESULT 4
AX003947 48 bp DNA linear PAT 24-AUG-2000
LOCUS
DEFINITION Sequence 7 from Patent WO923249.
ACCESSION AX003947
VERSION AX003947.1 GI:9927607
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 48)
AUTHORS Kessler, C., and Bartl, K.
TITLE Specific and sensitive method for detecting nucleic acids
JOURNAL Patent: WO 9923249-A 7 14-MAY-1999;

KESSLER CHRISTOPH (DE); BARTL KNOT (DE)
location/Qualifiers
1. .48
/organism='Homo sapiens',
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BASE COUNT 9 a 17 c 14 g 8 t
ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtcgtcagcctccagacc 21
|||||
Db 10 GTCGTCAAGCCTCCAGACC 30

RESULT 5
AX021565 48 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 3 from Patent WO924606.
ACCESSION AX021565
VERSION AX021565.1 GI:10044849
KEYWORDS
SOURCE Hepatitis C virus.
ORGANISM Hepatitis C virus.
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepadnavirus.
REFERENCE 1 (bases 1 to 48)
AUTHORS Kessler, C., Bartl, K., Habershausen, G., and Orum, H.
TITLE Specific and sensitive nucleic acid detection method
JOURNAL Patent: WO 9924606-A 3 20-MAY-1999;
KESSLER CHRISTOPH (DE); BARTL KNOT (DE); HABERHAUSEN GERD (DE);
ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES
source
1. .48
/organism='Hepatitis C virus',
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BASE COUNT 9 a 18 c 14 g 7 t
ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtcgtcagcctccagacc 21
|||||
Db 10 GTCGTCAAGCCTCCAGACC 30

RESULT 6
AX021566 48 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 4 from Patent WO924606.
ACCESSION AX021566
VERSION AX021566.1 GI:10044850
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 48)
AUTHORS Kessler, C., Bartl, K., Habershausen, G., and Orum, H.
TITLE Specific and sensitive nucleic acid detection method
JOURNAL Patent: WO 9924606-A 4 20-MAY-1999;
KESSLER CHRISTOPH (DE); BARTL KNOT (DE); HABERHAUSEN GERD (DE);
ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
FEATURES
source
1. .48
/organism='Homo sapiens',
/db_xref='taxon:9606'

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 21:20:54 ; Search time 1915.63 Seconds
(without alignments)
229.406 Million cell updates/sec

Title: US-10-037-990A-3

Perfect score: 21

Sequence: 1 gtcgtgcagcctccagagacc 21

Scoring table: OLIGO_NUC

Searched: 1797656 seqs, 10463268293 residues

Word size: 21

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database:

GenEmbl:
1: gb_ba:
2: gb_hg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vl:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_om:
21: em_or:
22: em_ov:
23: em_pat:
24: em_ph:
25: em_pl:
26: em_ro:
27: em_sts:
28: em_un:
29: em_vl:
30: em_hlg_hum:
31: em_hlg_inv:
32: em_hlg_other:
33: em_hlgo_inv:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB	ID	Description
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1	21	100.0	21	6	AX147016	AX147016 Sequence
c	21	100.0	27	6	BD0000273	BD0000273 Oligonucleotide
3	21	100.0	48	6	AX003946	AX003946 Sequence
4	21	100.0	48	6	AX003947	AX003947 Sequence
5	21	100.0	48	6	AX021565	AX021565 Sequence
6	21	100.0	48	6	AX021566	AX021566 Sequence
7	21	100.0	48	6	AX021575	AX021575 Sequence
8	21	100.0	48	6	AX021576	AX021576 Sequence
9	21	100.0	48	6	AX021631	AX021631 Sequence
10	21	100.0	48	6	AX021632	AX021632 Sequence

ALIGNMENTS

RESULT 1
AX147016
LOCUS AX147016 21 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 10 from Patent WO0137291.
ACCESSION AX147016
VERSION AX147016.1 GI:14346287
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 21)
AUTHORS Weindel, K., Riedling, M. and Geiger, A.
TITLE Magnetic glass particles, method for their preparation and uses
PATENT: WO 0137291-A 10 25-MAY-2001;
Roche Diagnostics GmbH (DE)
FEATURES
source location/Qualifiers
1..21
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide probe (HCV)."
modified_base 1
/note="Ruthenium3+-(tris-bipyridyl)-derivatisation"
BASE COUNT 3 a 9 c 6 g 3 t
ORIGIN

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QY 1 gtcgtgcagcctccagagacc 21
DB 1 gtcgtgcagcctccagagacc 21

RESULT 2
BD0000273/c 27 bp DNA linear PAT 31-JAN-2002
LOCUS BD0000273
DEFINITION Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof.
ACCESSION BD0000273
VERSION BD0000273.1 GI:18623352
KEYWORDS JP 2000279200-A/11.
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 27)
AUTHORS Lynen, J.M. and Gorman, K.M.
TITLE Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof
JOURNAL Patent: JP 2000279200-A 11 10-OCT-2000;
ORWHO CLINICAL DIAGNOSTICS INC
COMMENT OS Artificial Sequence
PN JP 2000279200-A/11
PD 10-OCT-2000
PF 03-FEB-2000 JP 2000032656